

GenCore version 5.1.4.p5_4578
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 7, 2003, 15:14:54 ; Search time 134.5 Seconds
(without alignments)
6443.584 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257

Perfect score: 6089

Sequence: 1 atgcgcgcacgcgggcct.....aagaagcagcaggggtctga 3252

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=framer-n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool/US0995830/runat_07052003_151447_6239/app_query.fasta_1.3399
-DB-A Geneseq_101002 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0995830.ecgn.1.1.226 @runat_07052003_151447_6239 -NCPU=3
-NO_XLPXY -NO_WMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_Geneseq_101002:.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	5704	93.7	1083	20	AA22426	Human brain specif
2	5698	93.6	1083	21	AA244778	Human Elk voltage
3	5697	93.6	1083	21	AA244779	Human Elk voltage
4	5696	93.5	1083	21	AA244780	Human Elk voltage
5	5695	93.5	1083	21	AA244835	Her94, a potassium
6	5695	93.5	1083	21	AA244835	Her94, a potassium
7	5688	93.4	1080	21	AA244781	Human Elk voltage
8	5675	93.2	1083	21	AA244904	Human ESK1 (hesk1)
9	5649.5	92.8	1082	21	AA244128	Monkey potassium c
10	2529.5	41.5	1107	21	AA244907	Human potassium ch
11	2515	41.3	1102	21	AA244907	Human potassium ch
12	2461.5	40.4	1017	20	AA244907	Rat ESK1 potassium
13	2347	38.5	457	21	AA244907	Human brain specif
14	1901	31.2	1311	22	AB61234	Human ESK1 (hesk1)
15	1832.5	30.1	542	21	AA244905	Drosophila melanog
16	1551	25.5	1159	20	AA244905	Human potassium ch
17	1551	25.5	1159	20	AA244905	Human cation chann
18	1551	25.5	1159	20	AA244905	Long QT syndrome a
19	1551	25.5	1159	22	AA244905	Human potassium ch
20	1551	25.5	1159	23	AA244905	Human eag-related
21	1550	25.5	1159	21	AA244905	Human ether-a-go-g
22	1533.5	25.2	1163	21	AA244905	Long QT syndrome a
23	1482	24.3	290	21	AA244905	Rat ESK1 potassium
24	1473.5	24.2	958	23	AA244905	Human potassium ch
25	1408.5	23.1	1196	23	AA244905	Human transporter
26	1387	22.8	1174	22	AB65304	Human transporter
27	1369	22.5	962	21	AB65304	Drosophila melanog
28	1369	22.5	962	21	AA244905	Rat ESK1 potassium
29	1358.5	22.3	989	21	AA244905	Human potassium io
30	1355	22.3	905	23	AA244905	Human potassium io
31	1334	21.9	988	23	AA244905	Human transporter
32	1332.5	21.9	988	22	AA244905	Human transporter
33	1332.5	21.9	988	22	AA244905	A human alpha-subu
34	1331	21.9	988	23	AB676165	Human potassium ch
35	1120.5	18.4	888	22	AA244905	Human ether a gogo
36	1046	17.2	855	20	AA244905	Human erg subfamll
37	817.5	13.4	626	20	AA244905	Drosophila melanog
38	792	13.0	154	21	AA244905	Human erg subfamll
39	655.5	10.8	377	22	AA244905	Rat ESK2 potassium
40	568.5	9.3	1245	22	AB111953	Human polypeptide,
41	566	9.3	1203	22	AB111953	Human cation chann
42	566	9.3	1203	23	AB111953	Human HCN4 protein
43	554	9.1	423	22	AB111953	Human hyperpolaris
44	550	9.0	142	22	AA244905	Human K channel ho
45	550	9.0	142	22	AA244905	Human excretory re
						Human kidney relat

ALIGNMENTS

RESULT 1

AA22426

ID AA22426 standard; Protein: 1083 AA.

XX AA22426;

AC AA22426;

DT 28-SEP-1999 (first entry)

DE Human brain specific potassium channel protein sequence.

DE Brain specific potassium channel; human; central nervous system disorder;

KW dementia; cerebral ischaemic sclerosis; therapy.

XX Homo sapiens.

XX WO9937677-A1.

XX PD.

XX 29-JUL-1999.

Thu May 8 08:49:37 2003

PF 20-JAN-1999; 99WO-JP00190.
 XX 04-DEC-1998; 98JP-0346198.
 PR 23-JAN-1998; 98JP-0011434.
 XX (YAMA) YAMANOUCHI PHARM CO LTD.
 PA Miyake A, Mochizuki S, Yokoi H;
 PI WPI; 1999-458683/38.
 XX N-PSDB; AAX84910.
 DR Potassium channel protein expressed specifically in brain tissue and
 PT method for its production
 PS Claim 1; Page 33-39; 63pp; English.
 XX This sequence is the potassium channel protein of the invention,
 CC that is expressed specifically in brain tissue. The protein is used to
 CC treat and investigate disorders of the central nervous system such as
 CC dementia and cerebral ischaemic sclerosis.
 XX SQ Sequence 1083 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 1083
 Score: 5704.00 Matches: 1083
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.68% Indels: 0
 DB: 20 Gaps: 0
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 QY 61 CGCTTCGAGCGGACGACAGTACTCTGCTGCTGGCGACGCCAGCGGGGCTCTTC 120
 DB 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
 QY 121 CGCTGGTCTACTGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 DB 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
 QY 181 ATGACGCGGGGCTGCT 240
 DB 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
 QY 241 CAACAGATCGCAAGGCCCTTGGACGACACAGAGTTCAAGCTGAGCTGATCTGCTAC 300
 DB 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuLeuLeuTyr 100
 QY 301 CGGAAGACGGGCTCCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 DB 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120
 QY 361 GGGGAGTGGCT 420
 DB 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
 QY 421 GGGCCGACACATGAAGGACAGAGTGGTGGCGGGCGGCGGCGGCGGCGGCGGCGGCGG 480
 DB 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgGlyGlyArgGlyGlyArgGlySer 160
 QY 481 AAAGCTTCAATGCCAACGGCGGGCGGAGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCG 540
 DB 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
 QY 541 CTGCAGAGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 600
 DB 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200

QY 601 AACTTGCCTGAGTACAAAGTAGCCGATCGGAAAGTCGCCCTTCATCTCTGTTGCACTGT 660
 DB 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuHisCys 220
 QY 661 GGGGCACTGAGCGCACCTGGATGGCTTCCTGCTGCCACACACTCTATGATGGCTGTC 720
 DB 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuAlaThrLeuTyrValAlaVal 240
 QY 721 ACTGTGCCCTACAGCGT 780
 DB 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
 QY 781 CCCAGCGT 840
 DB 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280
 QY 841 CGTACCACATTCGTCCTCAAGTCGGCGAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
 DB 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300
 QY 901 CACTAGCTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaLeuProPheAspLeuLeu 320
 QY 961 CATGCTTCAAGGTCACACTGTCTTCTGCGGCGGCTGTCTGTGTAACAGCTGCGCTGCTG 1020
 DB 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340
 QY 1021 CGCCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 DB 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
 QY 1081 ACAGTGTCTATGCGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 DB 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
 QY 1141 ATTGGCAGCGGAGATCGAGACGACGAGTCCGAGCTCGCTGAGATGGCTGGCTGCTGCTG 1200
 DB 381 IleGlyGlnArgGluIleGluSerGluSerGluLeuProGluIleGlyTrpLeuGln 400
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 QY 1261 AACAGCTCCGCGCAGAGTGACACTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1320
 DB 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 440
 QY 1321 GAGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 DB 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
 QY 1381 AGCAGCTCACCAGCTGGGCTTCGCAAGCTGTCTGCGGCGGCTTCTGCTGCTGCTGCTGCT 1440
 DB 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480
 QY 1441 TTCTCCATCTGCACCATGCTCATCGCGCTGATGACGCGGCTGATGACGCGGCTGTTGGG 1500
 DB 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValAlaPheGlyAsnVal 500
 QY 1501 ACGGCCATCATCCAGCGCATGTAGCCCGCGCTTCTGCTACCCAGCGCGCGCGCGCGC 1560
 DB 501 ThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAsp 520
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 QY 1621 TACTTCCAGGCGCGCTGGCGGTGAACATGGCATCGACCCAGCGCGAGTGTCTGCAGAGC 1680
 DB 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 560

QY 1681 CTCCCTGACGAGTGGCGCAGACATCGCATGCACTGCACAAAGGAGGTCTCTCAGCTG 1740
 Db 561 LeuProaspGluLeuArgAlaAspIleAlaMetHisLeuHisGluValLeuGlnLeu 580
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 Db 581 ProLeuPheGluAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
 QY 1801 GCCTTCTGACCGCGGCGAGTACCTCATCCACCAAGGAGTGCCTGCAGGCCCTCTAC 1860
 Db 601 AlaPheCysThrProGlyGluTyLeuLeuHisGlnGlyAspAlaLeuGlnAlaLeuTy 620
 QY 1861 TTTGCTGCTGCTGCTCATGAGGTGCTCAAGGTTGGCACCCTGCTCGCCATCTAGGG 1920
 Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaLeuGly 640
 QY 1921 AAGGCGACCTGATCGGCTGTAGCTGCGCGCGGAGAGGTGGTAAAGGCCAATGCC 1980
 Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgGluGlnValValLysAlaAsnAla 660
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 Db 661 AspValLysGlyLeuThrTyCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
 QY 2041 AGCTTGGCTGTACCCGAGTTTGGCCCGCGCTTACGTGCTGCTGCTGCTGCTGCTG 2100
 Db 681 SerLeuAlaLeuTyProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700
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 Db 701 SerTyAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720
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 QY 2761 GCATCGGAGAGGCG 2820

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 QY 3181 GAGATGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
 Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGluGly 1080
 QY 3241 ACAGGGGTC 3249
 Db 1081 ThrGlyVal 1083

RESULT 2

AAV44778
 ID AAY44778 standard; Protein; 1083 AA.

AC AAY44778;

XX
 DT 04-MAY-2000 (first entry)

XX Human Elk voltage gated potassium channel subunit monomer.

XX Voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;
 KW Kv superfamily; Bag family; ether a go-go; Elk subfamily; modulator;
 KW chromosome 12q13; resting potential; cell excitability; seizure;
 KW CNS; migraine; psychotic; anticonvulsant; neuroprotective;
 KW ion flux disorder; reporter molecule; detection; gene therapy;
 KW antileptane; cerebroprotective; antipsychotic.

XX Homo sapiens.

XX Key

XX Region 452..514 Location/Qualifiers

XX /label= P-S6_region

XX /note= "Pore-S6 region with conserved amino acids"

XX /label= Extended P-S6_region

XX /note= "Extended Pore-S6 region with conserved amino acids"

XX Misc-difference 965

XX /note= "Encoded by CGT"

XX WO200001819-A1.

XX 13-JAN-2000.

XX 30-JUN-1999; 99WO-US14944.

XX 01-JUL-1998; 98US-0091469.

XX 21-JAN-1999; 99US-0116621.

Thu May 8 08:49:37 2003

XX
PA (ICAG-) ICAGEN INC.
XX Jegla TJ, Wickenden A;
XX WPI: 2000-182114/16.
XX N-PSDB; AA250119.
XX Novel polynucleotides and polypeptides of human ELK, a voltage-gated
PT potassium channel subunit useful for treating ELK mis-expression and
PT to screen for inhibitors and activators of such channels
XX Claim 13; Page 62; 79pp; English.
XX The present sequence is the human ELK (hELK) polypeptide monomer,
CC comprising an alpha subunit of the voltage-gated potassium channel
CC (VGPCs). It is a member of the Kv (Voltage gated potassium) superfamily,
CC (VGPCs). It is a member of the Kv (Voltage gated potassium) superfamily,
CC Esg (ether a go-go) family and ELK subfamily of potassium channel
CC monomers. hELK gene is mapped to chromosome 12q13. It is isolated
CC from brain and maintains the resting potential and controls excitability
CC of the cell. It has anticonvulsant activity. The hELK polypeptide can be
CC neuroprotective and anticonvulsant activity. The hELK polypeptide can be
CC used to screen for modulators of VGPCs, that are useful for treating
CC abnormal ion flux disorders, CNS disorders such as migraines, hearing
CC and vision problems, seizures, psychotic disorders and to prevent
CC strokes. It can be used as a marker for diagnosis of diseases linked to
CC this gene and also as reporter molecule in detection systems. The
CC polynucleotide is useful for gene therapy, to rectify ELK expression.
XX
SQ Sequence 1083 AA;
Alignment Scores:
Pred. No.: 0 Length: 1083
Score: 5698.00 Matches: 1082
Percent Similarity: 99.91% Conservative: 0
Best Local Similarity: 99.91% Mismatches: 1
Query Match: 93.58% Indels: 0
DB: 21 Gaps: 0
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DB 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGTTTCGAGCGACGACAGTAACTCTGCTGGGACGACCCAGGTGGCGGCTCTTC 120
DB 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
QY 121 CCCGTGCTACTGCTGTGATGCTCTGTGACCTCAGCGGCTCTCCCGGCTGAGGTC 180
DB 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
QY 181 ATGCGGGGCTGCTGCT 240
DB 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
QY 241 CACAGATCGCAGGCGCCCTGGACGACACAGAGTTCAAGGCTGAGCTGATCTGTAC 300
DB 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuLeuTyr 100
QY 301 CGGAAGAGCGGCTCCGCT 360
DB 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120
QY 361 GGGAGGTGGCT 420
DB 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
QY 421 GGGCGGACAGTGAAGGACAGGAGTGGTGGCGGCGCGGATATGGCGGCGGACGATCC 480
DB 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgGlyGlyArgAlaArgSer 160

QY 481 AAAGGCTTCAATGCCAACCGCGGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
DB 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
QY 541 CTCGAGAAGCAGCCCAAGGCAAGCAGCAGCTCAATAAGGGGGTGTGGGGAAGAACCA 600
DB 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200
QY 601 AACTTGCTGAGTACAAAGTAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
DB 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
QY 661 GGGCGCTGAGCGCACCTGGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
DB 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
QY 721 ACTGTGCGCTACAGCGTGTGTGTGAGCAGCAGCAGGAGCGGCGGCGGCGGCGGCGG 780
DB 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
QY 781 CCCAGCGTCTGTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 840
DB 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280
QY 841 CGTACCACATTCGTGTCCAAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 900
DB 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300
QY 901 CACTAGCTCACACCTGCT 960
DB 301 HistyrValThrThrPheLeuLeuAspValIleAlaLeuProPheAspLeuLeu 320
QY 961 CATGCTTCAAGTCAAGTGTACTTCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
DB 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340
QY 1021 CGCCTGCTGCGCTGCT 1080
DB 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
QY 1081 ACAGTCTCATGGCGGCTGTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1140
DB 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
QY 1141 ATGCGGCGGCGGAGATCGAGACGACGAGATCGAGCTGCTGAGATTCGCTGGCTGCAG 1200
DB 381 IleGlyGlnArgGluLeuGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400
QY 1201 GAGCTGCGGCGGCGGAGTCTGAGACTCCCTTACTACTGCTGGGCGGCGGCGGCGGCGG 1260
DB 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420
QY 1261 AACAGCTCCGCGGCGGAGTGAACACTGACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1320
DB 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 440
QY 1321 GAGTGTGCGGCGGCGGCTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1380
DB 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
QY 1381 AGCAGCTCACCGGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1440
DB 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480
QY 1441 TTCTCCATCTGCACATGCTCTCATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1500
DB 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValAlaPheGlyAsnVal 500
QY 1501 ACGGCGCATATCCAGCGCATGTACGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1560
DB 501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520
QY 1561 CTGCGCGGCTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620

Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540
 QY 1621 TACTTCCAGGCCACCTGGCGGTGAACATGTCATCGACACACCGAGTGTCTGCAGACC 1680
 Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 560
 QY 1681 CTCCCTGACGAGCTCGCGCGAGACATCCCATGACACCTGACCAAGAGGTCTCTGCAGCTG 1740
 Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580
 QY 1741 CCACTGTTGAGGGCGCCAGCGCGGTGCTGGGGGACGTCTCTGGCCCTGGCGGCC 1800
 Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
 QY 1801 GCCTTCTGACCGCGCGGTGACTCTATCCACCAAGCGATGCGCCGCGAGCCCTCTAC 1860
 Db 601 AlaPheCysThrProGlyGlyTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
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 Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700
 QY 2101 AGCTACAACCTGGTGTCTGGGGAGGCTCTGACAGGTGACACACAGTGTGCTGCTGCTGCTGCT 2160
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 QY 2161 GACAATACCTTATGTCCAGCTGGAGGAGAGAGACAGATGGGAGCAGGCGCCACG 2220
 Db 721 AspAsnThrLeuMetSerThrLeuGluGlyLysGluThrAspGlyGluGlnGlyProThr 740
 QY 2221 GTCTCCCGAGCCAGCTGATGAGCCCTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
 Db 741 ValSerProAlaProAlaAspGluProSerProLeuLeuSerProGlyCysThrSer 760
 QY 2281 TCATCTCAGCTGCCAAGCTGTATCCCGAGTGTGACAGACAGACAGCCCGCTGCTAGGT 2340
 Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780
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 Db 781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800
 QY 2401 CCAGGCGCTTAGAGGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
 Db 801 ProArgAlaLeuGluGlyLeuArgLeuProMetProThrAsnValProProAspLeu 820
 QY 2461 AGCCCGAGGTGTAGATGTCATTAAGAGCGGTGTGGCTGGACAGCCCAAGTCTCT 2520
 Db 821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840
 QY 2521 TTCGCGTGGCGGCTGCTGCGCGGATGTAGCAGACAGCCCTTCCCTGAGCAGGAGC 2580
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 QY 2581 GGCTGTCTACTTCTCCATGGCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
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 QY 2641 CTTGCGAGCGGTGACAGAGTGTGACAGAGTGTGACAGAGTGTGACAGAGTGTGACAGAGTGTGAC 2700

Db 881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900
 QY 2701 TCACCTTCCAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
 Db 901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920
 QY 2761 GCATCGGAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
 Db 921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940
 QY 2821 GACACTGGGGCATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
 Db 941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960
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 QY 2941 CGCTCTCAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
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 QY 3001 GAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
 Db 1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020
 QY 3061 TCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
 Db 1021 SerGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040
 QY 3121 ACTGGAGAGCCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
 Db 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060
 QY 3181 GAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
 Db 1061 GluMetValLeuLeuGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080
 QY 3241 ACAGGGGTC 3249
 Db 1081 ThrGlyVal 1083

RESULT 3
 AAY44779
 ID AAY44779 standard; Protein; 1083 AA.
 XX
 AC AAY44779;
 XX
 DT 04-MAY-2000 (first entry)
 XX
 DE Human Elk voltage gated potassium channel monomer variant #1.
 KW Voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;
 KW Kv superfamily; Bag family; ether a go-go; Elk subfamily; modulator;
 KW chromosome 12q13; resting potential; cell excitability; seizure; marker;
 KW CNS; migraine; treat; hearing/vision problem; psychotic; anticonvulsant;
 KW ion flux disorder; reporter molecule; detection; gene therapy;
 KW antimigraine; cerebroprotective; neuroprotective; antipsychotic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 452..514
 FT /label= P-S6_region
 FT /note= "Pore-S6 region with conserved amino acids"
 FT Region 452..710
 FT /label= Extended_P-S6_region
 FT /note= "Extended Pore-S6 region with conserved amino acids"
 FT Misc-difference 1065
 FT /note= "Wild type Ile substituted with Val; Ile is
 FT stated to be located at 1064 in the specification"

Thu May 8 08:49:37 2003

XX WO200001819-A1.
 PN 13-JAN-2000.
 PD 30-JUN-1999; 99WO-US14944.
 XX 01-JUL-1998; 98US-0091469.
 PR 21-JAN-1999; 99US-0116621.
 XX (ICAG-) ICAGEN INC.
 PA Jegla TJ, Wickenden A;
 PI WPI; 2000-182114/16.
 DR Novel polynucleotides and polypeptides of human ELK, a voltage-gated
 PT potassium channel subunit useful for treating ELK mis-expression and
 PT to screen for inhibitors and activators of such channels
 PT
 XX Disclosure; Page -: 79pp; English.
 PS
 XX The present sequence is the human ELK (hELK) polypeptide variant #1,
 CC comprising an alpha subunit of the voltage-gated potassium channel
 CC (VGPCs). It is a member of the Kv (Voltage-gated potassium) superfamily,
 CC Eag (ether a go-go) family and ELK subfamily of potassium channel
 CC monomers. hELK gene is mapped to chromosome 12q13. It is isolated
 CC from brain and maintains the resting potential and controls excitability
 CC of the cell. It has antinigrane, cerebroprotective, antipsychotic,
 CC neuroprotective and anticonvulsant activity. The hELK polypeptide can be
 CC used to screen for modulators of VGPCs, that are useful for treating
 CC abnormal ion flux disorders, CNS disorders such as migraines, hearing
 CC and vision problems, seizures, psychotic disorders and to prevent
 CC strokes. It can be used as a marker for diagnosis of diseases linked to
 CC this gene and also as a reporter molecule in detection systems. The
 CC polynucleotide is useful for gene therapy, to rectify ELK expression.
 CC Note: The present sequence is not found in the specification, but is
 CC derived from hELK amino acid sequence found in page 62.
 XX
 SQ Sequence 1083 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 1083
 Score: 5697.00 Matches: 1081
 Percent Similarity: 99.91% Conservative: 1
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 93.56% Indels: 0
 DB: 21 Gaps: 0
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 Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
 QY 61 CGCTTCGACGGCAGCAGCAGTACTCTGCTGGGCGGCGGCGGCGGCGGCGGCGGCTTC 120
 Db 21 ArgPheAspGlyThrHisSerAsnThrPheLeuLeuGlyAsnAlaGluValLeuPhe 40
 QY 121 CCCGCTGCTACGCTGCTGCT 180
 Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
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 Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
 QY 241 CAACAGATCCGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 Db 81 GlnGlnIleArgGlyAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100
 QY 301 CGGAAGACGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
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 QY 361 GGGAGGTTGGCT 420
 Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
 QY 421 GGGCGGCGAGATGGAAGGAGACAGGTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 480
 Db 141 GlyProAspArgTyrPlysGluThrGlyGlyArgArgTyrGlyArgAlaArgSer 160
 QY 481 AAAGGCTTCAATGCCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 540
 Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
 QY 541 CTGCAAGCAGCCCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 600
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 QY 601 AACTTGCTGAGTACAAAGTAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 660
 Db 201 AsnLeuProGluTyrLysValAlaAlaLysLysSerPheLeuLeuLeuHisCys 220
 QY 661 GGGCAGCTGAGACCCACTGGGATGGCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
 Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheLeuLeuAlaThrLeuTyrValAlaVal 240
 QY 721 ACTGTGCGCTACAGCGT 780
 Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
 QY 781 CCCAGCGTCTGTGACCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 840
 Db 261 ProSerValCysAspLeuAlaValGluValLeuPheLeuAspIleValLeuAsnPhe 280
 QY 841 CGTACCATTGCTGCTCAAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 900
 Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300
 QY 901 CACTACGTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 Db 301 HistyrValThrThrThrPheLeuLeuAspValIleAlaLeuProPheAspLeuLeu 320
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 Db 341 ArgLeuLeuArgLeuLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValVal 360
 QY 1081 ACAGCTGCTATGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisThrPheValAlaCysValTrpPheTyr 380
 QY 1141 ATGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1200
 Db 381 IleGlyGlnArgGluIleGluSerGluSerGluLeuProGluIleGlyTyrPheLysGln 400
 QY 1201 GAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1260
 Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420
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 Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 440
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 Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
 QY 1381 AGCAGCTCACCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1440
 Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480

QY	1441	TTCTCCATCTGCACCATGCTCATCGCGCCCTGATGCACGGGTGGTGTGTTGGGAACGTG	1500
Db	481	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnVal	500
QY	1501	ACGGCCATCATCCAGCGCATAGCCCGCGCTTCTGTACCAACAGCCGACCGCCGAC	1560
Db	501	ThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAsp	520
QY	1561	CTGCGCGACTACATCCCGATCCACCGTATCCCCAAAGCCCTCAAGCAGCGCATGCTGGAG	1620
Db	521	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu	540
QY	1621	TACTTCCAGGCACCTGGCGGTCAACAATGGCATCGACACCAACGAGTGTCTGCAGAGC	1680
Db	541	TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer	560
QY	1681	CTCCCTGACGAGTTCGCGCAGACATCGCCATCCACTCCACACCGATGCTCGAGGTCT	1740
Db	561	LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu	580
QY	1741	CCACTGTTTGGCGGCGACCGCGCTCGCTCGCGGCACTGTCTGTGSCCTCGGGCCC	1800
Db	581	ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro	600
QY	1801	GCCTTCGTCACGCGCGGCGAGTACTCATCCACCAAGCGATGCCTCGAGGCCCTCTAC	1860
Db	601	AlaPheCysThrProGlyLysIleLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr	620
QY	1861	TTTGTCTGCTCTGGCTCCATGAGGTGCTCAAGGTGGACCGTGTCTGCCATCTCTAGGG	1920
Db	621	PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly	640
QY	1921	AAGGGCGACTGATGGCTGTGAGTGCCTCCCGCGGGAGCAGGTGGTAAAGGCCCAATGCC	1980
Db	641	LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValLysAlaAsnAla	660
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Db	661	AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp	680
QY	2041	AGCCTTGGCTGTACCCGAGTTTGCCCGCGCTTCAGTCTGTGGCTCCGAGGGAGCTC	2100
Db	681	SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu	700
QY	2101	AGCTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGTGGACACCACTCCCTGAGCGGC	2160
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QY	2221	GTCTCCCGACCCAGCTGATGAGCCCTCCAGCCCTGCTGCTGCCCTGGCTGCACCTCC	2280
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QY	2281	TCATCCTCAGTGCACAGCTGTATCCCCACGCTCGAACACGACCCCGGCTCGTCTAGT	2340
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Db	801	ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu	820
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QY	2521	TTCCGGCTGGCCAGTCTTGGCCGGAATGTAGCAGCAGCCCTCTCCCTGGACCAGAGC	2580
Db	841	PheArgValGlyGlnSerGlyProGluCysSerSerProSerProGlyProGluSer	860
QY	2581	GGCTGCTCAGTGTTCCTCCCATGGCCGACGAGGCAAGAAACACAGACACTGGACAAG	2640
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QY	2641	CTTCCGGCAGGGGTGCACAGAGCTGTACAGCAGGTGTGCAGATCGCGGAGGACTGCAG	2700
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QY	2701	TCACATTCGCCAGGCTGTCCACCTTGTCTGGCGCCCCACAGGGAGGTCGCTGCCCTCGG	2760
Db	901	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	920
QY	2761	GCATCGGAGAGGGCGCTGCCACGACGACACCTCCGGGCTTCTGCAGCCTCTGTGTGTG	2820
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QY	2821	GACACTGGGGCATCCTCTACTGCTGCAGCCCCCAGCTGGCTCTCTGTAGTGGGACT	2880
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Db	961	TrpProHisProAlaProGlyProProProLeuMetAlaProTrpProTrpGlyProPro	980
QY	2941	CGGCTCTCAGAGCTCCCTCGCTGGCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA	3000
Db	981	AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerSerAspSer	1000
QY	3001	GAGCCCCCTGCCCTCAGAGACCTCTCTCTGAGCCACGCCCTGCCCTCCCTCTCTCTCT	3060
Db	1001	GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro	1020
QY	3061	TCTGAGGAAGGGCTAGGACTGGGCCCGCAGACCTGTGAGCCAGCTGAGGCTACCAAGC	3120
Db	1021	SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer	1040
QY	3121	ACTGGAGAGCCCCACCAGGCTCAGGGGCTTGGCTTGGCTGGACCCCGCCAGCGCTG	3180
Db	1041	ThrGlyGluProProGlySerGlyLeuAlaLeuProTrpAspProHisSerLeu	1060
QY	3181	GAGATGGTCTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGACCCAGGAAGAGGC	3240
Db	1061	GluMetValLeuValGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly	1080
QY	3241	ACAGGGGGTC 3249	
Db	1081	ThrGlyVal 1083	
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ID	AA44780		
XX	AA44780 standard; Protein; 1083 AA.		
AC	AA44780;		
DT	04-MAY-2000 (first entry)		
XX	Human Elk voltage gated potassium channel monomer variant #2.		
DE	Voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;		
KW	Kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;		
KW	chromosome 12q13; resting potential; cell excitability; seizure; marker;		
KW	CNS; migraine; treat; hearing/vision problem; psychotic; anticonvulsant;		
KW	ion flux disorder; reporter molecule; detection; gene therapy;		
KW	antimigraine; cerebroprotective; neuroprotective; antipsychotic.		
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key Location/Qualifiers		


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Region      452..514
/label= P-S6_region
/note= "Pore-S6 region with conserved amino acids"
Region      452..710
/label= Extended_P-S6_region
/note= "Extended Pore-S6 region with conserved amino acids"
Misc-difference 1060
/note= "Wild type Leu substituted with Ile"

XX FT WO200001819-A1.
XX PD 13-JAN-2000.
XX PP 30-JUN-1995; 99WO-US14944.
XX PR 01-JUL-1998; 98US-0091469.
XX PR 21-JAN-1999; 99US-0116621.
XX PA (ICAG-) ICAGEN INC.
XX PJ Jegla TJ, Wickenden A;
XX PI WPI; 2000-182114/16.
XX DR
XX XX Novel polynucleotides and polypeptides of human ELK, a voltage-gated
XX PT potassium channel subunit useful for treating ELK mis-expression and
XX PT to screen for inhibitors and activators of such channels
XX PS Disclosure; Page -: 79pp; English.
XX XX The present sequence is the human ELK (hElk) polypeptide variant #2,
XX CC comprising an alpha subunit of the voltage-gated potassium channel
XX CC (VGPCs). It is a member of the Kv (Voltage gated potassium) superfamily,
XX CC Eag (ether a go-go) family and Elk subfamily of potassium channel
XX CC monomers. hElk gene is mapped to chromosome 12q13. It is isolated
XX CC from brain and maintains the resting potential and controls excitability
XX CC of the cell. It has antimigrane, cerebroprotective, antipsychotic,
XX CC neuroprotective and anticonvulsant activity. The hElk polypeptide can be
XX CC used to screen for modulators of VGPCs, that are useful for treating
XX CC abnormal ion flux disorders, CNS disorders such as migraines, hearing
XX CC and vision problems, seizures, psychotic disorders and to prevent
XX CC strokes. It can be used as a marker for diagnosis of diseases linked to
XX CC this gene and also as reporter molecule in detection systems. The
XX CC polynucleotide is useful for gene therapy, to rectify ELK expression.
XX CC Note: The present sequence is not found in the specification but
XX CC derived from hElk amino acid sequence found in page 62.
XX SQ Sequence 1083 AA;

Alignment Scores:
Pred. No.: 0 Length: 1083
Score: 5696.00 Matches: 1081
Percent Similarity: 99.91% Conservative: 1
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 93.55% Indels: 0
DB: 21 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x AAY44780 (1-1083)

QY 1 ATCCGGCCATCGGGGGCTCTCGGCGCTCAGAACACCTTCCTGGACACCATCGCTACG 60
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCGACGGCAGCCACAGTAACCTTCGTGGCCACGCCACAGTGGCGGGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
QY 121 CCGCTGTCTACCTGCTCTGATGGCTTCTGTGACCTTCACGGGGTCTCCGGGGCTGAGGTC 180
Db 41.ProValValIyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
QY 181 ATGCAGCGGGGGCTGTGCCTGCTCTCTCCCTTTATGGCCACAGCACCATCGCTCCGCG 240

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Db	61	MetGlnArgGlyCysAlaCysSerPheLeuTyrglyProaspThrSerGluLeuValArg	80
QY	241	CAACAGATCCGCAAGGCCCTCGAGCAGCACAAAGAGTCAAGGCTGAGCTGATCTCTGTAC	300
Db	81	GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTy	100
QY	301	CGGAGAGCGGCTCCCGTCTCTGGTGTCTCTGGATGTGATACCCATAAAGAATGAGAA	360
Db	101	ArgLysSerGlyLeuProPheTrpCysLeuLeuaspValIleProIleLysAsnGluLys	120
QY	361	GGGAGGTGGCTCTTCTAGTCTCTCACAGGACATCAGCAAAACCAAGAACCGAGGG	420
Db	121	GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly	140
QY	421	GGCCCGACAGATGGAAGAGAGAGTGTGGCCGGCCGCGATATGCGCGGCGCAGTCC	480
Db	141	GlyProAspArgTrpLysGluThrGlyGlyArgArgGlyArgGlyArgGlyArgGly	160
QY	481	AAAGGCTTCAATGCCAACCGCGGGGAGCCGGGCGGTGCTTACCACCTGTCCGGGCAC	540
Db	161	LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyHisLeuSerGlyHis	180
QY	541	CTGCAGAACGAGCCCAAGGCAAGCACAGCTCATTAAGGGGTCTTGGGAGAAACCA	600
Db	181	LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro	200
QY	601	AACTTGCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTCATCTGTGTGACATGT	660
Db	201	AsnLeuProGluTyLysValAlaIleArgLysSerProPheIleLeuLeuHisCys	220
QY	661	GGGCGCTGAGAGCCACTGGATGGCTTCATCTGCTGCCACACTCATGTGCTGCTGC	720
Db	221	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyValAlaVal	240
QY	721	ACTGTGCCCTACAGCTGTGTGTGAGCACACACGAGCCAGTCAGTCGCCGCGGCCG	780
Db	241	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260
QY	781	CCCAGCTCTGTGACCTGGCGTGGAGGTCTTTCATCTTACATTTGACATTTGCTGAATTC	840
Db	261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe	280
QY	841	CGTACCATCTGCTGCCAAGTCGGGCGAGTGTGTTGCCCAAAGTCCATTTGCCCTC	900
Db	281	ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu	300
QY	901	CACTAGCTCACCCTGCTCTCTGTGATGTATCGCAGCGCTGCCCTTTGACCTGCTA	960
Db	301	HisTyValThrThrTrpPheLeuLeuaspValIleAlaLeuProPheAspLeuLeu	320
QY	961	CATGCTTCAAGTCAACGTGTACTTCGGGGCCCATCTGTGTAAGAGCGTGCCTGCTG	1020
Db	321	HisAlaPheLysValAsnValTyPheGlyAlaHisLeuLeuLysThrValArgLeuLeu	340
QY	1021	CGCGTCTCGCGCTGTTCCGCGGTGGACCGGTACTCGCAGTACAGCGCGTGGTGGTG	1080
Db	341	ArgLeuLeuArgLeuLeuProArgLeuaspArgTySerGlnTySerAlaValValLeu	360
QY	1081	ACACTGCTCATGGCCGTGTGCCCTGTGCGGCACCTGGTGGCTGGCTGGTGGTTTAC	1140
Db	361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTy	380
QY	1141	ATTGGCCAGCGGAGATPCGAGAGCAGCGAATCCGAGCTCCCTGACATGGCTGGCTG	1200
Db	381	IleGlyGlnArgGluIleGluSerSerGluLeuProGluIleGlyTrpLeuGln	400
QY	1201	GAGTGGCCCGCGACTGGAGACTCCTACTACTCTGGTGGCGGAGGCGACCTGGAGGG	1260
Db	401	GluLeuAlaArgArgGluThrProTyTyTyLeuValIcIyArgArgProAlaGlyGly	420
QY	1261	AACAGCTCCGGCCAGGTGACAACACTGCAGCAGCAGGAGGCGCAACGAGCGGGCTG	1320

Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440
 QY 1321 GAGTGTGGGGGGCCCTGCTGGCAGCGCTACATCAGCTCCCTCTACTTCCACATC 1380
 Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
 QY 1381 AGCAGCTTCACACCGTGGGCTTGGCAACGTGTCGCCAACAGGACGACGAGGAGATC 1440
 Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480
 QY 1441 TTCCTCATCTGCACATGCTCATCGGCGCCCTGATGACGCGGTGGTGTGGGAAGCTG 1500
 Db 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValAlaPheGlyAsnVal 500
 QY 1501 AGGCGCATCATCCAGCGCATGATCCCGCGCTTCTGTACACACGCGCGCGAC 1560
 Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAsp 520
 QY 1561 CTGCGGAGCTACATCCCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620
 Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540
 QY 1621 TACTTCCAGCGCCACTGGGGGTGAACATGGCATCGACACACCGAGCTGTGCAGAGC 1680
 Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 560
 QY 1681 CTCCCTGACGAGCTGGCGGAGACATCGCATCGACCTGCACAGGAGTCTTCGACGTG 1740
 Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580
 QY 1741 CCACTGTTTGGAGCGCCAGCGCGCTCCCTCGCGGCACTGCTGTGGCCCTGCGGCCCC 1800
 Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
 QY 1801 GCCTTTGTGACCGCGGCGAGTACCTATCCACAGGAGTGCCTGAGGCCCTCTAC 1860
 Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
 QY 1861 TTTGTCTGCTTGGTCCATGAGGTGCTCAAGGTGGCAGCGTGTGCCCATCTAGAG 1920
 Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 540
 QY 1921 AAGGCGACCTCATCGCTGTGAGTGTGCCCGCGGAGCAGGTGTGAAGGCCAATGCC 1980
 Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 560
 QY 1981 GACGTGAAGGGCTGACGTACTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
 Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
 QY 2041 AGCCTTGGCTGTACCCGAGTTTGGCGGCTTCAAGGTGGCAGCGTGTGAAGGCCAATGCC 2100
 Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700
 QY 2101 AGCTACAACTGGTGTGGGGAGGCTCTCAGAGGTGGACACAGCTCCCTGAGCGGC 2160
 Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluAlaAspThrSerSerLeuSerGly 720
 QY 2161 GACAACTACCTTATGTCCAGCTGGAGAGAGAGAGAGATGGGAGCAGGCGCCACG 2220
 Db 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740
 QY 2221 GTCTCCCGACCGCAGCTGATGACCTTCCAGCCCTTCCAGCCCTTCCAGCCCTTCCAGCCCT 2280
 Db 741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760
 QY 2281 TCATCTCTCAGCTGCAGCTGCTATCCCGCTTCCAGCTGCGACACACCGCCCGCTGCTAGGT 2340
 Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780
 QY 2341 GGCAGAGGAGGCGCAGGCGGCGCTTGAAGGCTGAGGCTGCGCCCTCTGCTCCC 2400
 Db 781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800

QY 2401 CCACGGCGCTAGAGGGGCTACGGCTGCCCCCATGCCATGCAATGTGCCCCCAGATCTG 2460
 Db 801 ProArgAlaLeuGluGlyLeuArgLeuProMetProTrpAsnValProProAspLeu 820
 QY 2461 AGCCCCAGGGTAGTAGATGGCATTTGAAGACGGCTGTGGCTCGGACGACGACCAAGTCTCT 2520
 Db 821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840
 QY 2521 TTCCGCGTGGCGGCGCTGTGGCGGGAATGTAGCAGACGCCCCCTCCCTGGACGACGAGC 2580
 Db 841 PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer 860
 QY 2581 GGCCTGTCTACTGTTCCTCCATGGCGCCAGCGACGCAAGCAACACAGACACTGGACAAG 2640
 Db 861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880
 QY 2641 CTTCGCGAGCGGTGACAGAGCTGTACAGCAGGTGTGTGCAGATCCGCGAAGGACTGCAG 2700
 Db 881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900
 QY 2701 TCATTCGCGAGCGGTGTGACAGCTGTCTGCGCGCCACAGGAGGTTCCGTCGCCCTCGG 2760
 Db 901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920
 QY 2761 GCATCGGAGAGGCGCGTGCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820
 Db 921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940
 QY 2821 GACACTGGGCGATCCCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
 Db 941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960
 QY 2881 TGGCCCCACCCCTCGTCCGGGCGCTCTCCCTCATGCGACCCCTGGGCTGGGCTCCCTCC 2940
 Db 961 TrpProHisProAlaProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980
 QY 2941 GCGTCTCAGAGTCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
 Db 981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000
 QY 3001 GAGCCCCCTGCTCAGGAGACCTCTCTGAGCCCGACGACCCCTGCTCCCTCCCTCCCT 3060
 Db 1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020
 QY 3061 TCTGAGGAGGCGCTAGGACTGGGCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
 Db 1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040
 QY 3121 ACTGAGAGAGCGCCACCGAGGTGCGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
 Db 1041 ThrGlyGluProProProGlySerGlyLeuAlaLeuProTrpAspProHisSerIle 1060
 QY 3181 GAGATGCTGTATTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
 Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080
 QY 3241 ACAGGGGTC 3249
 Db 1081 ThrGlyVal 1083

RESULT 5
 AAY84835
 ID AAY84835 standard; Protein; 1083 AA.
 XX
 AC AAY84835;
 XX AC
 XX DT
 XX 08-AUG-2000 (first entry)
 DE Herg4, a potassium channel protein of the ERG family.
 XX Human; potassium channel protein; Herg4; human erg related gene 4;
 KW epilepsy; migraine; cell proliferation disorder; cancer;

QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCTTCTCTACACACAGCGCGCGAC 1560
DB 501 ThrAlaIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgSP 520
QY 1561 CTGCGGCTACATCCGATCCACCGATCCCAAGCCCTCAAGCAGCGCATGTGGAG 1620
DB 521 LeuArgSPtYrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540
QY 1621 TACTTCCAGGCCATCGGCGGTGAACATGGCATCGACACCGAGTGTGTGAGAGC 1680
DB 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer 560
QY 1681 CTCCCTGACGAGTGTGCGCGCAGACATCCCATGCCATGCCACGAGGTGTGTGAGTG 1740
DB 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580
QY 1741 CCACCTGTTGAGGGCGCGCGGCTGCTGCGGGGACGTCTCTGCGCCCTGCGGCC 1800
DB 581 ProLeuPheGluAlaLeuSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
QY 1801 GCCTTCTGACGCGCGGCGAGTACTCATCCACCAAGCGATGCCCTGCAGGCCCTCTAC 1860
DB 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
QY 1861 TTTTCTCTGCTGCTCCATGCGAGTGTCTCAAGGGTGGCACCGCTGCGCATCTAGGG 1920
DB 621 PheValCysSerGlyPheMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640
QY 1921 AAGGGCCACCTGTAGCTGTGAGCTGCCCGCGGGGAGAGGTGGTAAAGGCCAATGCC 1980
DB 641 LysGlyAspLeuIleGlyCysGluLeuProArgGluGlnValValLysAlaAsnAla 660
QY 1981 GAGCTGAAGGGGTGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
DB 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
QY 2041 AGCTTGGCGGTACCCCGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
DB 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyLeuLeu 700
QY 2101 AGCTACACCTGGTGTCTGGGGAGGCTGTGACAGGTGGACACCGCTGCTGCTGCTGCTGCT 2160
DB 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720
QY 2161 GACAATACCTTATGTCCAGCTGGAGGAGAGGACAGATGGGAGAGGCCCGCCACG 2220
DB 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740
QY 2221 GTCTCCCGCCAGCTGATGAGCCTCCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
DB 741 ValSerProAlaProAlaAspGluProSerProLeuLeuSerProGlyCysThrSer 760
QY 2281 TCATCTCAGCTGCCAAGTGTATCCCGACGTCCGACACCGCCCGCTGCTGCTGCTGCTGCT 2340
DB 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780
QY 2341 GGCAGAGGAGCCAGGCGGCGGCTTTGAGGCTGAGGCTGCGCCCTGCTGCTGCTGCTGCTGCT 2400
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QY 2401 CCACGGCGCTAGAGGGCTAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
DB 801 ProArgAlaLeuGluGlyLeuArgLeuProMetProTyrAsnValProProAspLeu 820
QY 2461 AGCCCGAGGTAGTAGTGGATTCAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
DB 821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840
QY 2521 TTCGCGTGGCGGCTAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
DB 841 PheArgValGlyGlnSerGlyProGlyCysSerSerSerSerSerSerSerSerSerSerSer 2640

QY 2581 GGCTCTCTCACTGTTCCCATGGCCCGCAGCGAGGCAAGCAACACACACACTGGACAAG 2640
DB 861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880
QY 2641 CTTGCGAGCGGTGACAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 2700
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DB 961 TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980
QY 2941 CGCTCTCAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
DB 981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000
QY 3001 GAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
DB 1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020
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QY 3121 ACTGAGAGCGCCCGCAGAGGCTGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
DB 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpPASPProHisSerLeu 1060
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DB 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGluGly 1080
QY 3241 ACAGGGGCTC 3249
DB 1081 ThrGlyVal 1083
RESULT 6
AAY44781
ID AAY44781 standard; Protein; 1083 AA.
XX
AC AAY44781;
XX
DT 04-MAY-2000 (first entry)
XX
DE Human Elk voltage gated potassium channel monomer variant #3.
XX
KW Voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;
KW kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;
KW chromosome 12q13; resting potential; cell excitability; seizure; marker;
KW CNS; migraine; treat; hearing/vision problem; psychotic; anticonvulsant;
KW ion flux disorder; reporter molecule; detection; gene therapy;
KW antimigrane; cerebroprotective; neuroprotective; antipsychotic.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 452..514
FT /label- P-S6_region
FT /note- "Pore-S6 region with conserved amino acids"
FT 452..710

Db	81	GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr	100
QY	301	CGAAAGAGCGGGCTCCGGTTCTGGTGTCTCGATGTGATACCCATAAAGAATGAGAA	360
Db	101	ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys	120
QY	361	GGGAGGTGGCTCTCTTCCTAGTCTCTCAAGGACATCAGCGAACAACAGAACCCGAGG	420
Db	121	GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly	140
QY	421	GGCCCCGACAGATGAAGAGACAGAGTGGTGGCGCGCGCATATGGCCGGCAGCATCC	480
Db	141	GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTrpGlyArgAlaArgSer	160
QY	481	AAAGGCTTCAATGCCAACACCGCGCGGAGCGGGCGCTGCTACCACTCTCCGGGCAC	540
Db	161	LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis	180
QY	541	CTGCAGAGACGCCAACGAGGCACCAAGCTCAATAGGGGTGTGTGGGAGAAACCA	600
Db	181	LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro	200
QY	601	AACHTGGCTGAGTACAAGTAGCGCCATCGGAAGTCCGCCCTTCATCCTGTTCGACTGT	660
Db	201	AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys	220
QY	661	GGGCGACTGAGAGCCACCTGGGATGGCTTCATCTGCTCGGCACACTCTATGTGGCTGTC	720
Db	221	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal	240
QY	721	ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGCGGAGCCAGCTCGCCCGCGGCCGG	780
Db	241	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260
QY	781	CCAGCGTCTGTGACTTGGCCGTGAGGTCCCTTCATCTTGCATGTGCTGTAATTTC	840
Db	261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe	280
QY	841	CGTACCACATTGGTCTCCAAGTCGGCGCAGGTGGTGTTCGCCCCAAAGTCCATTGGCCTC	900
Db	281	ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu	300
QY	901	CACTACGTCAACACCTGGTTCCTGCTGGATGTCATCGCAGCGGTGCCCTTTGACCTGCTA	960
Db	301	HisTyrValThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu	320
QY	961	CATGCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTCTGTGAGACGTGCGCTGCTG	1020
Db	321	HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu	340
QY	1021	CGCCTCTCGGCTGCTTCCGGCGTGGACCGGTACTCGCAGTACAGCGCGCTGGTGTCTG	1080
Db	341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu	360
QY	1081	ACACTGCTCATGGCCGTGTTCGCCCTCGCTCGCGACTGGGTTCGCTCGCTGTTTAC	1140
Db	361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380
QY	1141	ATTGGCCAGCGGAGATCGAGACGCGAATCCGAGCTGCCTGAGATTGCTGGCTGCAG	1200
Db	381	IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln	400
QY	1201	GAGCTGGCCCGCGACTGGAGACTCCTACTACTGTGGCGCGGAGCCAGCTGGAGGG	1260
Db	401	GluLeuAlaArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420
QY	1261	AACAGCTCCGGCCAGAGTGACAACCTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGCTG	1320
Db	421	AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu	440
QY	1321	GAGTGTCTGGGCGCGCTCGCTCGCGCAGCGCCTACATCACTCCCTCTACTTCGCACCTC	1380

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.41% Indels: 0
 DB: 21 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x AAY77738 (1-1080)

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 QY 70 GGCACGACAGTAACTTCGTCTGGCAACGCCAGAGTGGGGGCTCTCCCGCTGCTC 129
 DB 21 GlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPheProValVal 40
 QY 130 TACTGTCTCTGATGGCTTCTGTGACCTCAGGGGCTTCTCCGGGCTGAGGTACATCAGCGG 189
 DB 41 TyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluValMetGlnArg 60
 QY 190 GGCTGTGCTCTCTCTCTTATGGCCACACACCTAGTGTGCTCTCCCGCCCAACAGATC 249
 DB 61 GlyCysAlaCysSerPheLeuThrGlyProAspThrSerGluLeuValArgGlnGlnIle 80
 QY 250 CGCAAGCCCTGGAGCAGCACAAGAGTTCAAGGCTGAGTGTCTCTGATGATGATGATGATGATG 309
 DB 81 ArgLysAlaLeuAspGluHisGlyPheLysAlaGluLeuLeuLeuLeuLeuLeuLeuLeu 100
 QY 310 GGGTCTCCGCT 369
 DB 101 GlyLeuProPheThrCysLeuLeuAspValIleProIleLysAsnGluLysGlyGluVal 120
 QY 370 GCT 429
 DB 121 AlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGlyGlyProAsp 140
 QY 430 AGATGGAAGGACAGAGTGGTGGCGGGCGGCGATATGCGGGGCGACATGCAAGAGCTTC 489
 DB 141 ArgTrpLysGluThrGlyGlyArgArgTrpGlyArgAlaValLeuThrHisLeuGlnLys 160
 QY 490 AATGCCAACCGCGGCGGAGCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 549
 DB 161 AsnAlaAsnArgArgSerArgAlaValLeuThrHisLeuSerGlyHisLeuGlnLys 180
 QY 550 CAGCCCAAGGCAAGCACAAGCTCAATAAGGGGCTTTGGGAGAGAAACCAACTTCGCT 609
 DB 181 GlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyLysProAsnLeuPro 200
 QY 610 GAGTACAAAGTACGCCCATTCGGGAAGTGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 669
 DB 201 GluTrpLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCysGlyAlaLeu 220
 QY 670 AGAGCCACCTGGGATGGCT 729
 DB 221 ArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTrpValAlaValThrValPro 240
 QY 730 TACAGCGTGTGTGTGACAGCAGCAGCGGAGCCAGTGCCTCCCGCCCGCGCCAGCGTC 789
 DB 241 TyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyProSerVal 260
 QY 790 TGTGACCTGGCGGTGGAGTCT 849
 DB 261 CysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPheArgThrThr 280
 QY 850 TTCGTGTCTTCCAGTGGCGGCGGAGTGGTGTTCCTCCCAAGTCCATTTCCTCCACTAGCTC 909
 DB 281 PheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeuHisTrpVal 300
 QY 910 ACCACCTGGTCT 969
 DB 301 ThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeuHisAlaPhe 320
 QY 970 AAGGTCAACGTGTACTTCGGGGCGCCATCTGCTGAAGAGCGGTGCCTGCTCGCGCTGCTG 1029

anticonvulsant.
 Homo sapiens.

Key Location/Qualifiers
 Domain 212..239
 /note= "potential transmembrane domain S1"
 Domain 259..277
 /note= "potential transmembrane domain S2"
 Domain 297..320
 /note= "potential transmembrane domain S3"
 Domain 329..349
 /note= "potential transmembrane domain S4"
 Domain 356..378
 /note= "potential transmembrane domain S5"
 Modified-site 418
 /note= "potential N-glycosylation site"
 Modified-site 425
 /note= "potential N-glycosylation site"
 Modified-site 433
 /note= "potential N-glycosylation site"
 Domain 449..468
 /note= "potential pore-forming P domain"
 Modified-site 467
 /note= "potential N-glycosylation site"
 Domain 477..501
 /note= "potential transmembrane domain S6"
 Modified-site 496
 /note= "potential N-glycosylation site"
 Domain 601..668
 /note= "putative cyclic nucleotide binding domain (CNBD)"

W0200009534-A1.

24-FEB-2000.

13-AUG-1999; 99WO-US18556.

14-AUG-1998; 98US-0096570.

(ELAN-) ELAN PHARM INC.

Forsayeth JR, Zhao BB;

WPI: 2000-224270/19.

N-PSDB; AAZ87712.

Novel eag similar potassium channel polypeptide useful for treating various neurological, cardiovascular, musculoskeletal and proliferative disorders

Claim 3; Fig 1A-E; 52pp; English.

This represents a eag similar K+ channel (ESK) polypeptide (hESK1). The hESK1 protein can be expressed by standard recombinant methodology. The ESK polypeptide, polynucleotides and antibodies are useful for treating and diagnosing various potassium channel associated disorders such as neurological disorders, e.g. Alzheimer's disease, depression, anxiety, panic, obsessive-compulsive disorders, schizophrenia, Huntington's disease and Parkinson's disease, cardiovascular disorders, musculoskeletal disorders and hyperactivity disorders such as cancer. The ESK polynucleotide is also useful for synthesis of ESK and gene mapping. The polypeptide can be used in an assay to identify molecules such as synthetic drugs, can antibodies, peptides or other molecules which have an effect on the activity of the ESK channel.

Sequence 1080 AA;

Alignment Scores: 0 Length: 1080
 Pred. No.: 5688.00 Matches: 1080
 Score:

which is a member of ERG potassium channel family. This sequence is from a full length clone jtkba25d10 which was derived from monkey hippocampal library. ERG-LP1 is expressed exclusively in the brain. Highest expression is found in cortical regions, hippocampus, caudate and amygdala. The protein functions as a potassium channel modulator and anticonvulsant antidepressant.

CC neuroleptic and nootropic activities. The present sequence is
CC useful for treating several potassium channel mediated disorders (CNS
CC disorders) such as Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, epilepsy, depression, schizophrenic disorders and amnesia.
XX

SQ Sequence 1083 AA;

Alignment Scores:

Pred. No.: 0 Length: 1083
Score: 5675.00 Matches: 1078
Percent Similarity: 99.63% Conservative: 1
Best Local Similarity: 99.54% Mismatches: 4
Query Match: 93.20% Indels: 0
DB: 21 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x AAY44904 (1-1083)

QY 1 ATGCGGCGCATCGGGGCTCTGCGGCTCAGAACACCTTCTCGGACACCATCGCTAGG 60
DB 1 MetProAlaMetArgGlyLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCGACGGCACACAGTAACCTTCGTGGCAACGCCAGGTGGCGGGCTCTTC 120
DB 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
QY 121 CCGTGGTCTACTGCTGTGATGGCTCTGTGACCTCAGCGGCTTCTCCGGGCTGAGTTC 180
DB 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
QY 181 ATGACGGGGGCTGTGCTGCTCTGTGCTGTGACCTCAGCGGCTTCTCCGGGCTGAGTTC 240
DB 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
QY 241 CAACAGATCCGCAAGGCCCTGGACGACCAAGAGTTCAGGCTGAGCTGATCCTGTAC 300
DB 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100
QY 301 CGGAAGCGGGCTCCGCTTCTGTGTCTCTGTGATGATACCATCAAAAGTACGAAA 360
DB 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120
QY 361 GGGAGGTGGCTCTCTCTAGTCTCTCACAAAGGACATCAGCGAAACCAAGAACCGAGGG 420
DB 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
QY 421 GGGCCGACAGATGGAAGGACAGAGTGGTGGCGGCGCGCATATGCGCGGACGATCC 480
DB 141 GlyProAspArgTrpLysGluThrGlySerGlyArgArgTrpGlyArgAlaArgSer 160
QY 481 AAAGGCTCAATCCACCGCGCGGAGCGGGCGCTGCTTACCACTGTCCGGGCAC 540
DB 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
QY 541 CTGCAGAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTGGGGAGAACCA 600
DB 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200
QY 601 AACTTGCCTGAGTACAAAGTAGCGGCATCCGGAAGTCGCGCTTCATCCGTGTCAGTGT 660
DB 201 AsnLeuProGluTrpLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
QY 661 GGGGCGTACAGCCACTGGGATGGCTCATCTGCTCGCCACACTATGTGGTGTG 720
DB 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
QY 721 ACTGTGCCCTACAGCTGTGTGTGACACAGCAGCGGAGCCAGTCCCGCCCGCCG 780
DB 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
QY 781 CCCAGGCTGTGTGACCTGGCGGTGGAGTCCCTTTCATCTTGCATTTGTGCTGAATTC 840
DB 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280

QY 841 CGTACCACATTCGTGTCCCAAGTGGGCCAGGTGGTGTTCCTCCCAAGTCCATTGCTC 900
DB 281 ArgThrThrPheValSerLysSerGlyGlnValPheAlaProLysSerIleCysLeu 300
QY 901 CACTAGCTCACACCTCGTTCCTGCTGGATGTCATCGACGCTGCTTGGACCTGCTA 960
DB 301 HisTyrValThrThrPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320
QY 961 CATGCTTCAAGGTCAACGTACTTTCGGGGCCCATCTGCTGAAGACGGTGCCTGCTG 1020
DB 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340
QY 1021 CGCTGTGCTGCTGCTTCCGGGCTGGACCGGTACTCTCAGTACAGCGCGGTGGTGTG 1080
DB 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
QY 1081 ACACCTCTCATGCGCGGTTCGCTGCTGCGGCACTGGTGGCTGCTGCTGCTGCTTAC 1140
DB 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
QY 1141 AATGGCCAGCGGAGATCGAGACGAGCATCCGAGTCCCTGAGATTCGCTGGCTGGTGCAG 1200
DB 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400
QY 1201 GAGCTGGCGCGGCTGAGACTCCCTACTACTGTTGGGCGGAGGCGGAGCTGGAGGG 1260
DB 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValIleGlyArgProAlaGlyGly 420
QY 1261 AACAGCTCCGGCCAGAGTACAACTGCAGCAGCAGCAGCGGACGCGGAGCGGGCTG 1320
DB 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440
QY 1321 GAGTGTGCGGCGGCGCTGCTGCGGAGCGCTACATCCTCCTCTACTTCTGCTGCTGCT 1380
DB 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
QY 1381 AGCAGCTCACAGCGTGGGCTTCGCGCAACGTTCGCGCAACACGACGACGAGAGATC 1440
DB 461 SerSerLeuThrSerValIleGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480
QY 1441 TTCCTCATCTCCAGCATCTCATCGCGCGCTGATGACGCGGTGCTGTTGGGACGCTG 1500
DB 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnVal 500
QY 1501 ACGGCCATCATCCAGCGCATGTAGCGCGCGCTGCTTGTACACAGCGCGGCGGAC 1560
DB 501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520
QY 1561 CTGCGGCTACATCCGCTACCGCATCCCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620
DB 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540
QY 1621 TACTTCCAGGCGCCTGGGCGGTGAACAATGGCATCGACACACCGAGCTCTCGCAGAGC 1680
DB 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer 560
QY 1681 CTGCTGACGAGTGGCGGAGACATCCCATGACCTGCACAAAGGAGGTCTCTGACGCTG 1740
DB 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580
QY 1741 CCAGTGTTCGAGCGGCGGCGGCTGCTGCGGGGACTGTCTGTGGCCCTCGGCGCC 1800
DB 581 ProLeuPheGluAlaLaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
QY 1801 GCCTTCTGACGCGGCGGAGTACCTCATCCCAAGCGCATGCGCTGCGAGGCGCTCTAC 1860
DB 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
QY 1861 TTTGTCTGCTCTGCTCCATGGAGGTGCTCAAGGTGGCAGCTGCTCGCCATCTTAGG 1920
DB 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640
QY 1921 AAGGCGACCTGTATCGCTGTGAGCTGCTGCGGCGGAGCAGGTGGTAAAGGCCAATGCC 1980

[illegible]

are known to cause four human diseases: episodic ataxia with myokymia;
 CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
 CC As potassium channels are critical components of virtually all cells,
 CC it is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS)
 CC disorders. Nucleotides encoding K-Hnov proteins may be used for
 CC identifying homologous or related proteins and the DNA sequences encoding
 CC them. They may be used to produce compositions that modulate the
 CC expression and function of the K-Hnov protein and in studying the
 CC biochemical pathways associated with it. They may also be used for the
 CC recombinant production of K-Hnov protein in fermentation cultures.
 CC Additionally, such nucleotides may be used in gene therapy protocols for
 CC the treatment of diseases associated with abnormal potassium channels.
 XX

SQ Sequence 1082 AA;

Alignment Scores: 0 Length: 1082
 Pred. No.: 5649.50 Matches: 1076
 Score: 99.35% Conservativity: 0
 Percent Similarity: 99.35% Mismatches: 6
 Best Local Similarity: 92.78% Indels: 1
 Query Match: 20 Gaps: 1
 DB:

US-09-965-830-1_copy_6_3257 (1-3252) x AAY34128 (1-1082)

QY 1 ATGCGGCGCATCGGGGCTCTGCGGCTCAGAACACTTCTTGGAGACCATCGCTACG 60
 DB 1 MetProAlaMetArgGlyLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
 QY 61 CGCTTCGACGCGCACAGTAACCTCGTGTGGGCAACGCCAGTGGCGGGCTCTTC 120
 DB 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaSer---GlyGlyAlaLeu 39
 QY 121 CCCGTGGTCTACTGCTGTGATGGTCTGTGACCTCAGGGCTTCTCCGGGCTGAGGTC 180
 DB 40 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 59
 QY 181 ATGCAGCGGGCTGTGCTGCTCTCTGCTGATGATACCCATCAAGAGTGGTCTGTCGC 240
 DB 60 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 79
 QY 241 CAACAGATCCGCAAGGCCCTGAGCAGCAGACAGAGTCAAGGCTGAGCTGATCCTGTAC 300
 DB 80 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuLeuTyr 99
 QY 301 CGGAAGCGGGCTCCGCTTCTGCTGCTGCTGATGATACCCATCAAGAGTGGTCTGTCGC 360
 DB 100 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 119
 QY 361 GGGAGTGGCTCTCTTCTTCTCTCAGAGACATCAGCGAAACCAAGACCGAGGG 420
 DB 120 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 139
 QY 421 GGGCCCGACAGATCGAAGGAGACAGTGGTGGCGGCGCGATGATGCGCGGACGATCC 480
 DB 140 GlyProAspArgTrpLysGluThrGlyGlyArgArgTyrGlyArgAlaArgSer 159
 QY 481 AAAGGCTTCAATCCAAACCGCGCGAGCGCGGCTGCTTACACCTGTCTGGGCGAC 540
 DB 160 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 179
 QY 541 CTCAGAAGCAGCCAGGCGACAGCAAGCTCAATGAAGGGGTGTTGGGAGAACCA 600
 DB 180 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 199
 QY 601 AACTTGCCTGAGTACAAAGTAGCGGCATCCGGAAGTTCGCGCTTCACTCTGTTGCACTGT 660
 DB 200 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheLeuLeuHisCys 219
 QY 661 GGGGCTGAGAGCCACTCGGGATGCTTCACTGCTGCCACACTATGTGGCTGTC 720
 DB 220 GlyAlaLeuArgAlaThrTrpAspGlyPheLeuLeuAlaThrLeuTyrValAlaVal 239

QY 721 ACTGTCCCTACAGCGTGTGTGTGACACAGCAGCGGAGCCAGTCCGCCCGCGGCCG 780
 DB 240 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 259
 QY 781 CCCAGCGTGTGTGACCTGGCCGCTGAGGTCCTCTTCTCATCTTGCATTTGCTGCAATTC 840
 DB 260 ProSerValCysAspLeuAlaValGluValPheLeuLeuAspIleValLeuAsnPhe 279
 QY 841 CGTACACATTCGTGTCGAAGTGGCCAGGTGGTGTGTTGCCCAAGTCCATTGGCTC 900
 DB 280 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 299
 QY 901 CACTAGTCCACCATCTGCTTCTGCTGGATGTATCGCAGCGCTGCCCTTGTACCTGCTA 960
 DB 300 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 319
 QY 961 CATGCTTCAAGGTCAACGTGTACTTTCGGGGCCCATCTCTGTAAGAGCGTGGCCCTGTG 1020
 DB 320 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 339
 QY 1021 CGCTGTGCTGCTGCTTCCGGGCTGAGCCGTACTCGCAGTACAGCGCGCTGGTGTGCTG 1080
 DB 340 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 359
 QY 1081 ACATGCTCATGCGCGTGTTCCTCGCTGCTGCGGCACACTGGGTGCGCTGCTGTGTTTAC 1140
 DB 360 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 379
 QY 1141 ATTGCCAGCGGAGATCGAGAGCAGCGAATCCGAGTCCGTGAGATTGGCTGGCTGACAG 1200
 DB 380 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 399
 QY 1201 GAGTGGCGCGCGACTGGAGACTCCCTACTACTCTGGTGGCGGAGCGCCAGCTGAGGG 1260
 DB 400 GluLeuAlaAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 419
 QY 1261 AACAGCTCCGCGCAGAGTGACAACTGACAGCAGCAGCAGCGGCCCAACGGGAGCGGGTG 1320
 DB 420 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 439
 QY 1321 GAGTGTGGCGCGCGCTGCTGCGCAGCGCTACATCACCTCCCTCTACTTCCACTC 1380
 DB 440 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 459
 QY 1381 AGCAGCTCACAGCGTGGCTTGGCAACGTGTCGCCAACACACGACCGAGAGATC 1440
 DB 460 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 479
 QY 1441 TTCTCCATCTGCACCATCTCTCATCGGCGCTGATGACAGCGGTGGTGTGTTGGGAACGTG 1500
 DB 480 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnVal 499
 QY 1501 ACGGCCATCATCCAGCGCATGTACCGCGCGCTTCTGTATACCACAGCGCGCCAGCGCGAC 1560
 DB 500 ThrAlaIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 519
 QY 1561 CTGCGGCACTACATCCCGCATCCCGTATCCCAAGCCCTCAAGCAGCGCATGCTGAG 1620
 DB 520 GlnArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 539
 QY 1621 TACTTCCAGCGCCACTGGCGGTGAACATGGCATCGACACACCGAGCTGCTGCAGAGC 1680
 DB 540 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 559
 QY 1681 CTCCCTGACAGCTGCGCGGAGACATCGCATCGCATCGACACACCGAGCTGCTGCAGCTG 1740
 DB 560 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 579
 QY 1741 CCAGTGTTCAGCGCGCCAGCGGGCTGCTGGGCGACTGTCTGTGGCTCGCGGCC 1800
 DB 580 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 599

Db	960	TrpProHisProArgGlyProGlyProProProLeuMetalaProArgProTrpGlyPro	979
QY	2941	GGTCTCAGAGCTCCCTGGCTCGAGCCACAGCTTCTTGAGACTCCACCTCAGACTCA	3000
Db	980	AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer	999
QY	3001	GAGCCCCCTGGCTCAGAGACACTCTGCTTGAGCCACGACCCCTGCTCCCTCCTCCT	3060
Db	1000	GluProProAlaSerGlyAspLeuGlySerGluProSerThrProAlaSerProProPro	1019
QY	3061	TCTGAGAAGGGCTAGGACTGGGCCCCCAGAGGCTGTGAGCAGGCTGAGGCTACACAGC	3120
Db	1020	SerGlnGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer	1039
QY	3121	ACTGGAGAGCCCCACACAGGGTCAGGGGCTGGGCTTGCCCTGGGAGCCCCACAGCCTG	3180
Db	1040	ThrGlyGluProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu	1059
QY	3181	GAGATGGTGCTATTGGCTGCCATGCTTGCCACAGTCCAGTGGACCCAGAGAAAGGC	3240
Db	1060	GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGluGly	1079
QY	3241	ACAGGGGCTC 3249	
Db	1080	ThrGlyVal 1082	
RESULT	10		
AAV44907	ID	AAV44907 standard; Protein; 1107 AA.	
XX	AC	AAV44907;	
XX	DT	18-MAY-2000 (first entry)	
XX	DE	Human potassium channel molecule ERG-LP2 full-length protein.	
XX	KW	Human; potassium channel molecule; ERG-like protein 2; ERG-LP2;	
KW	KW	neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;	
KW	KW	neuroleptic; nootropic; treatment; CNS disorder; central nervous system;	
KW	KW	potassium channel mediated disorder; epilepsy; Alzheimer's disease;	
KW	KW	Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia;	
XX	OS	Chromosome 3p21.3-24.3.	
XX	OS	Homio sapiens.	
XX	Fi	Key	Location/Qualifiers
FT	Domain	295..535	
FT	FT	/note= "Transmembrane region cyclic nucleotide gated	
FT	FT	channel domain"	
FT	Modified-site	320	
FT	FT	/note= "N-glycosylated"	
FT	Modified-site	409	
FT	FT	/note= "N-glycosylated"	
FT	Modified-site	439	
FT	FT	/note= "N-glycosylated"	
FT	Modified-site	468	
FT	FT	/note= "N-glycosylated"	
FT	Modified-site	617	
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FT	Modified-site	687	
FT	FT	/note= "N-glycosylated"	
FT	Modified-site	821	
FT	FT	/note= "N-glycosylated"	
FT	Modified-site	953	
FT	FT	/note= "N-glycosylated"	
FT	Modified-site	63..65	
FT	FT	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site	126..128	
FT	FT	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site	159..161	
FT	FT	/note= "Protein kinase C phosphorylation site"	
FT	Modified-site	216..218	

QY	481	---AAAGGCTTCAATGCCAACCGCGCGGAGCGCGCTGCTCTACCACTGCTCGCGG	537
Db	157	GlyThrHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly	176
QY	538	CACCTGAGAGAGCCAGGCGACACAGCTCAATAGGGGGTGTGGGAGAAA	597
Db	177	HisLeuGlnArgGluLysAsnLysLeuLysIleAsnAsnValPheValAspLys	196
QY	598	CCAAACTGCTGAGTACAAAGTAGCCGATCCGAGTCCGCGCTTCATCTGTCAC	657
Db	197	ProAlaPheProGluTyrLysValSerAspAlaLysLysSerLysPheIleLeuLeuHis	216
QY	658	TGTGGGCACTGAGAGCCACTCGGATGGCTTCATCTGCTCGCCACACTCTATGGCT	717
Db	217	PheSerThrPheLysAlaGlyTrpAspTrpLeuIleLeuAlaThrPheTyrValAla	236
QY	718	GTCACCTGTCCTACAGCGTGTGTGAGCAGACAGCGGAGCCAGTCCGCGCGGCG	777
Db	237	ValThrValProTyrAsnValCysPheIleGlyAsnAspLeuSerThrThrArgSer	256
QY	778	CGCGCCAGCGTGTGACCTGGCGGTGAGGTCTCTTCATCCTTGACATGCTGTAAT	837
Db	257	---ThrThrValSerAspIleAlaValGluIleLeuPheIleAspIleIleLeuAsn	275
QY	838	TTCGTCACCATCTGCTCCAAAGTCGCGGCGAGGTGTGTGCCCCAAAGTCCATTGC	897
Db	276	PheArgThrThrTyrValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCys	295
QY	898	CTCCACTACGTACACCATCTGCTGCTGTGATGTCATCGCAGCGCTGCCCTTTGACCTG	957
Db	296	IleHisTyrValThrThrPheIleIleAspLeuIleAlaLeuProPheAspLeu	315
QY	958	CTACATGCTTCAAGGTCAAGCTACTTCCGGGGCCATCTGCTGAAAGCGGTGGCGCTG	1017
Db	316	LeuTyrAlaPheAsnValThrValSerLeuValHisLeuLeuLysThrValArgLeu	335
QY	1018	CTGCGCTGCTGCGCTGCTCCGGCGGTGAGCGGTACTCGCAGTACAGCGCGGTGTG	1077
Db	336	LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal	355
QY	1078	CTGACACTGCTCATGCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1137
Db	356	LeuThrLeuLeuMetSerPheAlaLeuLeuAlaHisTrpMetAlaCysIleIrrPyr	375
QY	1138	TACATTGGCCAGCGGAGATCGAGACAGCAATCCGAGTCCGCTGAGATTGCTGGCTG	1197
Db	376	ValIleGlyLysMetGluArgGluAspAsnSerLeuLeuLysTrpGluValGlyTrpLeu	395
QY	1198	CAGGAGCTGGCGCGGCTGAGTCCCTACTACTACTCTGCTGGCGGCGGAGCCAGCTGA	1257
Db	396	HisGluLeuGlyLysArgLeuLeuSerProTyrTyr	407
QY	1258	GGGAACAGCTCCGCGCAGAGTGACAACTGACAGCAGCAGCGAGCGGAGCCACGCGGG	1317
Db	408	GlyAsnAsnThr	411
QY	1318	CTGGAGCTGTGGCGCGCGCTGCTGCGCAGCGCTTACATCCTCTACTTCGCA	1377
Db	412	---LeuGlyGlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThr	428
QY	1378	CTCAGCAGCTCACAGCGTGGCTTCGCGCAAGTGTCCGCCAACGACGACCGAGAAG	1437
Db	429	LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys	448
QY	1438	ATCTCTCCATCTGCACCATGCTCATCGCGCGCTGATGACCGCGGTGTGTGGGAAC	1497
Db	449	IlePheSerIleCysThrMetLeuIleGlyAlaLeuMethHisAlaLeuValPheGlyAsn	468
QY	1498	GTACGCGCCATCATCCAGCGCATGTAGCGCGCGCTTCTGTACACACCGCAGCGCGC	1557
Db	469	ValThrAlaIleIleGlnArgMetTyrSerArgTyrSerLeuTyrHisThrArgThrLys	488

Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMet 80
 QY 241 CAACAGGCTCCGAGCCCTGACGACGACACAGGAGTTCACGGCTGAGCTGATCTGTGAC 300
 Db 81 LeuGlnIleGluSerLeuGluGlnValGluPheLysGlyGluIleMetPheTyr 100
 QY 301 CGAAGAGGGGCTCCGCTTCCTGCTCTCCCTGATGATACCCATAAAGAAAGAGAA 360
 Db 101 LysLysAsnGlyAlaProPheThrPysLeuLeuAspIleValProIleLysAsnGluLys 120
 QY 361 GGGAGGCTGCT 417
 Db 121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140
 QY 418 GGGGGCCCGACAGATGGAAGAGACAGAGTGTGTGGCGCGCGATATGGCGGGCACGA 477
 Db 141 ThrSerGluAspLysLysGluAspArgAlaLysGlyArgSerArgAlaGly 157
 QY 478 TCCAAAGGCTCAATGCCAACCGCGGCGGAGCGCGGCTGTCTTACACCTGTCCGGG 537
 Db 158 ---SerHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 176
 QY 538 CACCTGCAGAGCAGCCCAAGGCGACAGCAAGCTCAATAAGGGGTGTGTGGGAGAA 597
 Db 177 HisLeuGlnArgGluLysAsnLysLysLysLysLysLysLysLysLysLysLys 196
 QY 598 CCAACTTCCTGAGTACAAAGTAGCGGCATCCGGAAGTGGCCCTCTATCTCTGTGTCAC 657
 Db 197 ProAlaPheProGluTyrLysValSerAspAlaLysLysSerLysPheIleLeuLeuHis 216
 QY 658 TGTGGGCGACTGAGACCGACCTGGGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 717
 Db 217 PheSerThrPheLysAlaGlyTyrPaspTyrPheLeuLeuAlaThrPheTyrValAla 236
 QY 718 GTCACTGTGCTTACAGCGT 777
 Db 237 ValThrValProTyrAsnValCysPheIleGlyAsnLysPheLeuSerThrThrArgSer 256
 QY 778 CCGCCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
 Db 257 ---ThrThrValSerAspIleAlaValGluIleLeuPheIleIleAspIleIleLeuAsn 275
 QY 838 TTCCTGACACATTCGT 897
 Db 276 PheArgThrThrTyrValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCys 295
 QY 898 CTCACCTACCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
 Db 296 IleHisTyrValThrThrThrPheIleAspLeuIleAlaLeuProPheAspLeu 315
 QY 958 CTACATCCCTCAAGGTCAAGTGTACTTCGGGGCCCATCTGCTGGAAGCGGTGCGGCTG 1017
 Db 316 LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLeuLysThrValArgLeu 335
 QY 1018 CTGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077
 Db 336 LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal 355
 QY 1078 CTGACACTGCTATGCGCGT 1137
 Db 356 LeuThrLeuLeuMetSerMetPheAlaLeuAlaHisTrpMetAlaCysIleTyrTyr 375
 QY 1138 TACATTGGCGAGGGAGATCGAGAGCGGAATCCGAGCTGCTCGAGTTGGCTGTGCTGTG 1197
 Db 376 ValIleGlyLysMetGluArgLysAspAsnSerLeuLeuLysTrpGluValGlyTrpLeu 395
 QY 1198 CAGGAGCTGCCCGCCGCTGAGACTCCCTTACTTACTTACTTACTTACTTACTTACTTACT 1257
 Db 396 HisGluLeuGlyLysArgLeuGluSerProTyrTyr 407
 QY 1258 GGGAAACAGCTCCGGCCAGAGTGACAACACTGACGACGACGAGCGGACGAGCGGCGGG 1317
 Db 408 GlyAsnAsnThr 411

QY 1318 CTGGAGCTGCTGGGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1377
 Db 412 -----LeuGlyGlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThr 428
 QY 1378 CTCACGAGCTCACCAGGCTGGGCTCGGCAACGCTGCGCCCAACACGACGACGAGAG 1437
 Db 429 LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys 448
 QY 1438 ATCTTCTCTCATCTGCACCATCTCATCGCGCGCTGATCGACGCGGTGTGTGTGGAA 1497
 Db 449 IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn 468
 QY 1498 GTGACGCGCATCATCGACGCGCATGTACGCGCGCGCTTCTGTACACACGCGCACGCG 1557
 Db 469 ValThrAlaIleIleGlnArgMetTyrSerArgTyrSerLeuTyrHisThrArgThrLys 488
 QY 1558 GACCTCGCGACTACATCCGATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATCTGCTG 1617
 Db 489 AspLeuLysAspPheIleArgValHisHisLeuProGlnGlnLeuLysGlnArgMetLeu 508
 QY 1618 GAGTACTTCCAGCCACCTGGGCGGTGAACATGGCATCGACACCGAGCTGTGTCAG 1677
 Db 509 GluTyrPheGlnThrThrTyrSerValAsnAsnGlyIleAspSerAsnGluLeuLys 528
 QY 1678 AGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATCGACATCGACACAGGAGTCTGTCAG 1737
 Db 529 AspPheProAspGluLeuArgSerAspIleThrMetHisLeuAsnLysGluIleLeuGln 548
 QY 1738 CTCCACTGTGTGAGCGGCGCACCGCGGTGCTGCGGGCAGCTGCTGTGCGCCCTGCGG 1797
 Db 549 LeuSerLeuPheGluCysAlaSerArgGlyCysLeuArgSerLeuSerLeuHisIleLys 568
 QY 1798 CCGCCTTCTGCGACGCGGCGGAGTACCTCATCCACAGCGCATGCGCTGCGAGCGCTC 1857
 Db 569 ThrSerPheCysAlaProGlyGluTyrLeuLeuArgGlnGlyAspAlaLeuGlnAlaIle 588
 QY 1858 TACTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1917
 Db 589 TyrPheValCysSerGlySerMetGluValLeuLysAspSerMetValLeuAlaIleLeu 608
 QY 1918 GGAAGGCGCACCTGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1977
 Db 609 GlyLysGlyAspLeuIleGlyAlaAsnLeuSerIleLysAspGlnValIleLysThrAsn 628
 QY 1978 GCGACCTGAAGGCGCTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2037
 Db 629 AlaAspValLysAlaLeuThrTyrCysAspLeuGlnCysIleIleLeuLysGlyLeuPhe 648
 QY 2038 GACAGCTTGGCTGTACCCGAGTTGCGCGGCTTACGTGCTGCTGCTGCTGCTGCTGCTGCT 2097
 Db 649 GluValLeuGlyLeuTyrProGluTyrAlaHisLysPheValGluAspIleGlnHisAsp 668
 QY 2098 CTCAGCTACACCTGGTGTGCTGGG-----GGAGGCTCT 2130
 Db 669 LeuThrTyrAsnLeuArgGluGlyHisGluSerAspValIleSerArgLeuSerAsnLys 688
 QY 2131 GCAGAGTGGACACACCTCCCTGAGCGCGGACAAATACCTTATGCTCCACGCTG----- 2184
 Db 689 SerThrValProGlnAlaGluProLysGlyAsnGlySerIleLysLysArgLeuProSer 708
 QY 2185 -----GAGGAGAAGGACAGATGGGAGGAGGCGCCACGCTGCTCCCGACGCCCA 2235
 Db 709 IleValGluAspGluGluGluGluValGluGluGluGluThrThrSerLeuSerPro 728
 QY 2236 GCTGATGAGCCCTCCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2295
 Db 729 IleTyrThrArgGlySerSerValSerHisSerLysLysThrGlySerSerLysSerTyr 748
 QY 2296 AAGTGTATATCCACGCTCGA-----ACAGCACCC-----CGTCTCT 2334
 Db 749 LeuGlyLeuSerLeuLysGlnLeuThrSerGlyThrValProPheHisSerProIleArg 768

QY 2335 CTAGTGGCAGAGGAGGAGCCAGGAGGAGGCTTTGAAGGCTGAGGCTGGCCCTCT 2394
Db : : : : :
Db 769 ValSerSerAlaAsnSerPro-----LysThrLysGlnGluAlaAspProPro 784
QY 2395 GCTCCCGCCAGGCGCTAGAG-----GGCTACGCTGCCCCCATGCGCATGAAT 2445
Db : : : : :
Db 785 AsnHisGlyThrArgLysGlnLysAsnLeuLysValGlnLeuCysSerLeuGlyThrAla 804
QY 2446 GTGCCCGCCAGATCTAGCGCCAGGAGTAGATGAGCATTAAGACAGGCTGTGCTCGGAC 2505
Db : : : : :
Db 805 GlyThrProGluLeuSerProArgLysValAspGlyLeuGluAspGlyAsnSerSerGlu 824
QY 2506 CAGCCCAAG-----TTCTTCTTCCGCTGGCCAGCTGCGCCGGAATGTAGCAGCAGCC 2562
Db : : : : :
Db 825 GluThrGlnThrPheAspPheGlySerGluGlnLeuArgProGluProArgLysSerPro 844
QY 2563 TCCCTGTGACACAG-----AGCGGCTGCTCAGCTGTTCCCATGCGCCAGCAGAG 2613
Db : : : : :
Db 845 SerLeuGlyGluSerGluLeuGlyAlaAlaPheLeuPheile-----Lys 859
QY 2614 GCAAGGACACA---GACACACTGACAGCTTCGGCAGCGGTGACAGAGTGTACAGAG 2670
Db : : : : :
Db 860 AlaGluGluThrLysGlnGlnLeuAsnLysLeuAsnSerGluValThrThrLeuThrGln 879
QY 2671 CAGGTGCTCAGATGGGAGGAGTGCAGTCACTTCGCCAGGCTGTGCAGCTGTGCTCG 2730
Db : : : : :
Db 880 GluValSerGlnLeuGlyLysAspMetArgSerLeuMetGlnLeuLysGluAsnLeuLeu 899
QY 2731 GCGCCCGCCAGGAGGCTCGGCTCGGCTCGGAGGCGGCGGCGGCGGCGGCGGCGG 2790
Db : : : : :
Db 900 SerProGlnGlnProSerGlnPheCysSerLeuHisProThrSerLeuCysProSerArg 919
QY 2791 ACCTCCGGGCTTCTGACGCTCTGTGTGGACACTGGGGCTGCTCTCTCTCTCTCTCT 2850
Db : : : : :
Db 920 GluSerPheGlnThrArg-----ValSerTrpSerAlaHisGlnProCysLeuHis 936
QY 2851 CCCCAGCT-----GGCTGTGCTTGTAGTGGGACTTGGCCCGCCAC 2889
Db : : : : :
Db 937 LeuGlnAlaAsnGlyAlaHisLeuTyrrHisGlyAsnValThrSerAspLeuTrp----- 954
QY 2890 CCTCGTGGGGCTTCTCCCTCATGCGACCCCTGGCTGGGCTGGGCTGGGCTGGGCT 2949
Db : : : : :
Db 955 -----SerValAspProSerLeuValGlySerAsnProGlnArgThrGluAlaHisGlu 972
QY 2950 AGCTCCCGC----- 2958
Db : : : : :
Db 973 GlnSerProValAspSerGluLeuHisHisSerProAsnLeuAlaTyrrSerProSerHis 992
QY 2959 -----TGGCTCGAGCCACA 2973
Db : : : : :
Db 993 CysGlnValIleGlnGluGlyHisLeuGlnPheLeuArgCysIleSerProHisSerAsp 1012
QY 2974 GCTTCTGGACCTCCACCTCAGACTCAGAGCCCTCGCTCAGGAGACCTCTGCTCTGAG 3033
Db : : : : :
Db 1013 ThrThrLeuThrProLeuGlnSerIleSerAlaThrLeuSerSerValCysSerSer 1032
QY 3034 CCCAGCACCT-----GCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3081
Db : : : : :
Db 1033 SerGluThrSerLeuHisLeuValLeuProSerArgSerGluGluGlySerIleThrHis 1052
QY 3082 GGGCCCGCAGAGCTGTGAGCAGGCTGAGCTACACACTGGAGACCCCGCCAGGAGG 3141
Db : : : : :
Db 1053 GlyProValSerSerPheSerLeu-----GluAsnLeuProGly 1065
QY 3142 TCAGGGGCGCTGGCTTGGCTGGGAC 3168
Db : : : : :
Db 1066 Ser-----TrpAsp 1068

RESULT 12
AAY22427
ID AAY22427 standard; Protein; 1017 AA.
XX
AC AAY22427;

XX 28-SEP-1999 (first entry)
XX Human brain specific potassium channel protein sequence.
DE Brain specific potassium channel; human; central nervous system disorder;
KW dementia; cerebral ischaemic sclerosis; therapy.
XX Homo sapiens.
OS WO9937677-A1.
PN 29-JUL-1999.
PF 20-JAN-1999; 99WO-JP00190.
XX 04-DEC-1998; 98JP-0346198.
PR 23-JAN-1998; 98JP-0011434.
XX (YAMA) YAMANOUCHI PHARM CO LTD.
PA Miyake A, Mochizuki S, Yokoi H;
PI WPI; 1999-458683/38.
XX N-PSDB; AAX84911.
DR Potassium channel protein expressed specifically in brain tissue and
PT method for its production
XX Claim 1; Page 44-49; 63pp; English.
PS This sequence is the potassium channel protein of the invention,
CC that is expressed specifically in brain tissue. The protein is used to
CC treat and investigate disorders of the central nervous system such as
CC dementia and cerebral ischaemic sclerosis.
XX Sequence 1017 AA;
SQ
Alignment Scores:
Pred. No.: 4.57e-152 Length: 1017
Score: 2461.50 Matches: 538
Percent Similarity: 59.19% Conservative: 119
Best Local Similarity: 48.47% Mismatches: 245
Query Match: 40.43% Indels: 208
DB: 23 Gaps: 23
US-09-965-830-1_COPY_6_3257 (1-3252) x AAY22427 (1-1017)

QY 1 ATGCCCGCCATCGGGGCTCTCTGCGCTCAGACACCTTCTCTGGACACCATCGCTACG 60
Db : : : : :
Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCGAGCGCCACACAGTAACCTCGTGGCGCAACGCCCGGCTGCTTC 120
Db : : : : :
Db 21 ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnGlyThrArgGlyPhe 40
QY 121 CCGCTGGTCTACTGCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db : : : : :
Db 41 ProIleValTyrrCysSerAspGlyPheCysGluLeuThrGlyTyrrGlyArgThrGluVal 60
QY 181 ATGACGCGGGCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db : : : : :
Db 61 MetGlnLysThrCysSerCysArgPheLeuTyrrGlyProGluThrSerGluProAlaLeu 80
QY 241 CAACAGATCCGAGCGGCTGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 300
Db : : : : :
Db 81 GlnArgLeuHisLysAlaLeuGluGlyHisGlnGluHisArgAlaGluLeuCysPheTyrr 100
QY 301 CGGAGAGCGGGCTCCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db : : : : :
Db 101 ArgLysAspGlySerAlaPheTrpCysLeuLeuAspMetMetProIleLysAsnGluMet 120
QY 361 GGGGAGGTGGCT 420

					
Db	121	GlyGluValIleValLeuPheLeuPheSerPheLysAspIleThrGlnSerGlySerProGly	140				
QY	421	--GGCCCGCAGATGAAGAAGACAGGTGGTGCCTGCCGCGCCCATATGCCGGCACCA	477				
Db	141	LeuGlyProGln-----			-GlyGlyArgGlyAspSerAsnHisGluAsn	154	
QY	478	TCCAAGGC-----			-TTCAATGCCAACCGCGCGCGAGACC	516	
Db	155	SerLeuGlyArgArgGlyAlaThrTrpLysPheArgSerAlaArgArgSerArgThr	174				
QY	517	GTGCTTACCACACTGCCGGCACCTGCAGAAGACAGCCAAAGCAACAAGCTCAAT	576				
Db	175	ValLeuHisArgLeuThrGlyHisPheGlyArgArgGlyGlnGlyMetLysAlaAsn	194				
QY	577	AAGGGGTGTTGGGAGAAAACAACTTGCTGAGTACAAGTAGCCGCATCCGGAAG	636				
Db	195	AsnAsnValPheGluProLysProSerValProGluTyLysValAlaSerValGlyGly	214				
QY	637	TCGCCCTTCACTCTGTGCACGTGGGGCAGTGAAGCCACTGGGATGCCTTCATCCTG	696				
Db	215	SerArgCysLeuLeuLeuHisTyrrSerValSerLysAlaIleTrpaspGlyLeuIleLeu	234				
QY	697	CTGCCACACTCTATGTGCTCTCACTGTGCCCTACACGCTGTCTGTGACACAGCAGG	756				
Db	235	LeuAlaThrPheTyrrValAlaValThrValProTyrrAsnValCysPheSerGlyAsp	254				
QY	757	GAGCCAGTCCCGCCGCGCGCCGACGCTGTGACCTGGCGGTGAGGTCCTCTTC	816				
Db	255	AspThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGluMetLeuPhe	274				
QY	817	ATCCTTGACATTGTGTAATTTCGTACCATTCGTGTCCAAAGTCGGCCAGGTGGT	876				
Db	275	IleLeuAspIleIleLeuAsnPheArgThrThrTyrrValSerGlnSerGlyGlnValIle	294				
QY	877	TTTGCCCCAAGTCCATTGGCTCCACTAGCTACACCACTGGTTCCTGCTGGATGTCATC	936				
Db	295	SerAlaProArgSerIleGlyLeuHisTyrrLeuAlaThrTrpPhePheIleAspLeuIle	314				
QY	937	GCAGCGTGCCTTTGACCTGTACATGCCTTCAAGTCAAGTGTACTTCGGGGCCCAT	996				
Db	315	AlaAlaLeuProPheAspLeuLeutyrrIlePheAsnIleThrValThrSerLeuValHis	334				
QY	997	CTGCTGAAGACGTGGCGCTGTGGCGCTGCCTGCCTTCCTCCGCGCTGACCGGTAC	1056				
Db	335	LeuLeuTyrrValArgLeuLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuTyrr	354				
QY	1057	TCGCAGTACAGCCGCTGGTGTGTGACACTGCTATGCGCGGTGTTCGCGCTGCTCGCAC	1116				
Db	355	SerGlnCysSerAlaValIleValLeuThrLeuLeuMetSerValPheAlaLeuLeuAlaHis	374				
QY	1117	TGGTTCGCTCGCTCTGTGTTTTACATTTGCCACGCGGAGATCGAGACAGCAATCCGAG	1176				
Db	375	TrpMetalacysIleIleTyrrValIleGlyArgArgGluMetGluAlaAsnAspProLeu	394				
QY	1177	CTGCCTGAGANTGGCTGTGTCAGGAGCTGGCGCGCGCTGGAGACTCCCTACTACTG	1236				
Db	395	LeuTrpaspIleGlyTrpLeuHisGluLeuGlyLysArgLeuGluValProTyrr-----	412				
QY	1237	GTGGCGCGGAGCCAGCTGGAGGGAACACTCCGCGCAGAGTGCACACTGCAGCAGCAGC	1296				
Db	412	-----	412				
QY	1297	AGCGAGGCCAACGGAGCGGGGTGGAGTGTCTGGCGCGCGCTGCTCGCAGCGCCTAC	1356				
Db	413	-----ValAsnGlySer-----	426				
QY	1357	ATCACCTCCCTCTACTTCGCACCTCAGCAGCCTCACACGCTGGGTTCGCAAGCTGCC	1416				
Db	427	IleAlaAlaLeuTyrrPheThrLeuSerSerLeuThrSerValGlyPheGlyAsnValCys	446				
QY	1417	GCCAACCGGACCGGAGAAGATCTTCTCCATCTGCACCATGCTCATCGCGCCCTGATG	1476				

Db	447	AlaAsnThrAspAlaGluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMet	456
QY	1477	CAGCGCGTGTGTTTGGGAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCGCTTT	1536
Db	467	HisAlaValAlaPheGlyAsnValThrAlaIleIleGlnArgMetTyrSerArgArgSer	486
QY	1537	CTGTACCACAGCGCAGCGCGACCTGCGGACTATATCCGCATCCACCGTATCCCAAG	1596
Db	487	LeuTyrHisSerArgMetLysAspLeuLysAspPheIleArgValHisArgLeuProArg	506
QY	1597	CCCTCAAGCAGCGCATGTGTGAGTACTTCCAGGCCACTGGCGGTGACAAATGGCATC	1656
Db	507	ProLeuLysGlnArgMetLeuGluTyrPheGlnThrThrTrpAlaValAsnSerGlyIle	526
QY	1657	GACACCACCGAGCTGTCAGAGCCCTCCTGTACGAGCTGCGCGAGACATCGCATCGAC	1716
Db	527	AspAlaAsnGluLeuLeuArgAspPheProAspGluLeuArgAlaAspIleAlaMetHis	546
QY	1717	CTGCACAAAGGAGTCTGTGAGCTGCCACTGTTGAGCGCGCAGCGCGCTGCTCGCGG	1776
Db	547	LeuAsnArgGluIleLeuGlnLeuProLeuPheGlyAlaAlaSerArgGlyCysLeuArg	566
QY	1777	GCATGTCTCTGGCCCTGGCGCGCGCTTCTGCACCGCGCGGAGTAGCTCATCCACCAA	1836
Db	567	AlaLeuSerLeuHisIleLysThrSerPheCysAlaProGlyGluTyrLeuLeuArgArg	586
QY	1837	GGCGATCCCTCGAGGCCCTCTACTTTGTCTCTCTGCTCCATGGAGGTGCTCAAGGT	1896
Db	587	GlyAspAlaLeuGlnAlaHisTyrTyrValCysSerGlySerLeuGluValLeuArgAsp	606
QY	1897	GGCACCGTGTCCGCATCTCTAGGAAGCGGACGTATCGCTGTGAGCTGCCCGCGCGG	1956
Db	607	AsnMetValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyAlaAspIleProGluPro	626
QY	1957	GAGCAG-----CTGGTAAAGCCCAATGCCGACGTG	1986
Db	627	GlyGlnGluProGlyLeuGlyAlaAspProAsnPheValLeuLysThrSerAlaAspVal	646
QY	1987	AAGGGCTGACGTACTGCGTCTGACAGTCTGTCAGCTGGCTGGCTCCACGACGCTT	2046
Db	647	LysAlaLeuThrTyrCysGlyLeuGlnGlnLeuSerSerArgGlyLeuAlaGluValLeu	666
QY	2047	CGCGTGTACCCGAGTTGTCGCCGCTTCAGTCTGCTGCTCCGAGGGAGCTCAGCTAC	2106
Db	667	ArgLeuTyrProGluTyrGlyAlaAlaPheArgAlaGlyLeuProArgAspLeuThrPhe	686
QY	2107	AACCTGGGTGCTGGGGAGCGCTCTGCAGAGGTGGACACAGCTCCCTG-----	2154
Db	687	AsnLeuArgGlnGlySer-----AspThrSerGlyLeuSerArgPheSer	701
QY	2155	-----ACGGCGCACANTACC	2169
Db	702	ArgSerProArgLeuSerGlnProArgSerGluSerLeuGlySerSerAspLysThr	721
QY	2170	CTTATGTCACGCTGGAGGAGAGGAGACAGATGGGAGCGGCCCCACGCTCTCCCCA	2229
Db	722	LeuProSerIle-----ThrGluAlaGluSerGly-----AlaGluPro	734
QY	2230	GCCCGAGTGTATGAGCCCTCCAGCCCGCTGCTGCCCTGGCTGACCTCTCATCTCATC	2289
Db	735	GlyGlyGlyProArgProArgProArgProLeuLeuLeuProAsnLeuSerProAlaArgPro	754
QY	2290	GCTGCCAAGCTG-----	2301
Db	755	ArgGlySerLeuValSerLeuLeuGlyGluLeuProProPheSerAlaLeuValSer	774
QY	2302	-----CTATCCCAACGTCGAACAGACAGCCCGCGCTGCTGTAGTGGGAGAGGGAGG	2352
Db	775	SerProSerLeuSerProSerLeuSer-----ProAlaLeuAlaGlyGlnGlyHis	791
QY	2353	CCAGCAGGGCAGGGGCTTTGAGGCTGAGGCTGGCGCCCTCTGCTCCCGCAGGGCCCTA	2412
Db	792	-----SerAlaSerProHisGlyProProArgCysSer	802

1063	QY	TACAGCGCGTGGTCTGCACACTGCTCATGGCGGTCTCGCCCTGCTCGCGCACTGGGTC	1122
141	Db	TyrSerAlaValValLeuThrLeuLeuMetAlaValPheAlaLeuAlaHisTrpVal	160
1123	QY	GCCTCGCTGTTTACATTGGCCAGCGGAGATCGAGACAGCGAATCCGAGCTGCCT	1182
161	Db	AlaCysValTrpPheTrpIleGlyGlnArgGluIleGlnSerSerGluSerGluLeuPro	180
1183	QY	GAGATTGGCTGGCTCCAGGAGCTGGCCCGGAGCTGGAGACTCCCTACTGCTGGGC	1242
181	Db	GluIleGlyTrpLeuGlnGluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGly	200
1243	QY	CGAGGCCAGCTGGAGGAGACAGCTCGGCGCAGAGTGACAACTGCAGCAGCAGCAG	1302
201	Db	ArgArgProAlaGlyGlyAsnSerSerGlyGlnSerAspAsnCySerSerSerGlu	220
1303	QY	GCCAAAGGAGCGGGCTGGAGCTGCTGGGGGGCGGCTCGCTGGCGAGCGCCTACATCACC	1362
221	Db	AlaAsnGlyThrGlyLeuGluLeuGlyGlyProSerLeuArgSerAlaTyrIleThr	240
1363	QY	TCCTCTACTTCGCACACTCAGCAGCCTCACCAGCGTGGCTTCGGCAACCTGTCCGCCAAC	1422
241	Db	SerLeuTyrPheAlaLeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsn	260
1423	QY	ACGGACACGAGAAGACTCTCTCCATCTGCACCATGCTCATCGCGCCCTGATGCACGCG	1482
261	Db	ThrAspThrGluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAla	280
1483	QY	GTGGTGTTTGGGAAGCTGACGCGCCATCATCCAGCGCATGTACCGCCGCGCTTCTGTAC	1542
281	Db	ValValPheGlyAsnValThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyr	300
1543	QY	CACAGCCGACGCGGACCTCGCGGACTACATCCGCATCCACCGTATCCCAAGCCCTC	1602
301	Db	HisSerArgThrArgAspLeuArgAspTyrIleArgIleHisArgIleProLysProLeu	320
1603	QY	AGCAGCGCATCTCGGAGTACTTCCAGGCCACCTGGCGGTGAACATGCATCGACACACC	1662
321	Db	LysGlnArgMetLeuGluTyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThr	340
1663	QY	ACCGAGCTCTCGAGCGCTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCGAC	1722
341	Db	ThrGluLeuLeuGlnSerLeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHis	360
1723	QY	AAGGAGTCTCTGACGTGCCACTGTGTTGAGCGGCCACCGCGCTGCCCTCGCGGCACTG	1782
361	Db	LysGluValLeuGlnLeuProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeu	380
1783	QY	TCCTCGGCCCTCGGCCCGCCCTTCGACGCCGGCGGAGTAGTACCTCATCCACCAAGCGCAT	1842
381	Db	SerLeuAlaLeuArgProAlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAsp	400
1843	QY	GCCTCGAGGCCCTCTACTTGTCTGTCTGGCTCCATGGAGGTGCTCAAGGTGGCACC	1902
401	Db	AlaLeuGlnAlaLeuTyrPheValCysSerGlySerMetGluValLeuLysGlyGlyThr	420
1903	QY	GTCTCGCCATCTTAGGGAAGCGCCACTGTATCGCTGTGTAGCTGCCCGCGGGGAGCAG	1962
421	Db	ValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyCysGluLeuProArgArgGluGln	440
1963	QY	GTGGTAAAGGCCAATCCGACAGCTGAAGGGGCTGAGCTACTCGCTCTGCAG	2013
441	Db	ValValLysAlaAsnAlaAspValLysGlyLeuThrTyrCysValLeuGln	457
RESULT 14			
ABB61234	ID	ABB61234 standard; Protein; 1311 AA.	
XX	XX	ABB61234;	
AC	XX		
XX	XX		
DT	DT	26-MAR-2002 (first entry)	

QY	301	CGGAAGACGGCGCTCCCGTCTCGTGTCTCCCTGGATGTGATACCCATAAAGATGAGAA	360
Db	127	LysLysGluGlyAlaProPheIrpCysLeuPheAspIleValProIleLysAsnGluLys	146
QY	361	GGGGAGGTGGCTCTCTTCTAGTCTCTCACAGGACATCAGCGAAACAAG	411
Db	147	ArgAspValValLeuPheLeuAlaSerHisLysAspIleThrHisThrLysMetLeuGlu	166
QY	411	-----	411
Db	167	MetAsnValAsnGluGluCysAspSerValPheAlaLeuThrAlaAlaLeuLeuGlyAla	186
QY	412	-----AACCGAGG	420
Db	187	ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyLeuProGlyLeuGly	206
QY	421	GGCCCC-----GACAGATGAAGAGAGACAGTGTGTGCCGCGCGATATGGCCGG	471
Db	207	GlyProAlaAlaSerAspGlyAspThrGluAlaGlyGluGlyAsnAsnLeuAspValPro	226
QY	472	GCAGATCCAAAGCTTCATATGCCAACGGCGGGAGCCGGCGCTGCTTACCACCTG	531
Db	227	Ala-----GlyCysAsnMetGlyArgArgSerArgAlaValLeuTyrGlnLeu	243
QY	532	TCCGGGCACCTGCAGAGACGACCCCAAGGGC---AAGCACAAAGTCATTAAGGG	582
Db	244	SerGlyHisTyrLysProGluLysGlyGlyValLysThrLysLeuLysLeuGlyAsnAsn	263
QY	583	---GTGTTTGGGAGAACCAACTCCCTGAGTACAAAGTAGCCGCCATCCCGAAGTCG	639
Db	264	PheMetHisSerThrGluAlaProPheProGluTyrLysThrGlnSerLysLysSer	283
QY	640	CCCTCATCCTGTGCACCTGTGGGCACTGAGAGCCACCTGGGATGCTTCATCCTGCTC	699
Db	284	ArgLeuIleLeuProHisTyrGlyValPheLysGlyLeIrpAspTrpValIleLeuVal	303
QY	700	GCACACTATGTGGTGTCACTGTCCCTACAGCGTGTGTGTGACAGCAGCAGCGGAG	759
Db	304	AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAlaAspArg	323
QY	760	CCAGTGCCTGGCGCGCGCCACCGCTGTGACCTGGCCGTGGAGTCTCTTCAATC	819
Db	324	GlnThr-----LysValSerAspValIleValGluAlaLeuPheIle	337
QY	820	CTTGACATTGTGCTGAATTCCTGATACACATTGCTCCAAAGTCGGCCAGTGGTGT	879
Db	338	ValAspIleLeuLeuAsnPheArgThrThrPheValSerArgLysGlyGluValSer	357
QY	880	GCCCAAGTCCATTGGCTCCACTACGTCACACCTGGTCTCTGCTGGATGTCATCGCA	939
Db	358	AsnSerLysGlnIleAlaIleAsnTyrLeuArgGlyTrpPheAlaLeuAspLeuLeuAla	377
QY	940	GGCTGCGCTTTGACCTGCTACATCCCTTCAGGTCAAGTGTACTTCGGG-----	990
Db	378	AlaLeuProPheAsp-----HisLeuTyrAlaSerAspLeuTyrAspGlyGluAspSer	395
QY	991	---GCCCATCTGCTCAAGACGGTGGCGCTGCTGGCCCTGCTCGGCTGTCTCCGGCGTG	1047
Db	396	HisIleHisLeuValLysLeuThrArgLeuLeuArgLeuAlaArgLeuLeuGlnLysIle	415
QY	1048	GACCGGTACTCGCAGTACAGCGCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1107
Db	416	AspArgTyrSerGlnHisThrAlaMetIleLeuThrLeuLeuMetPheSerPheThrLeu	435
QY	1108	CTCGGCACTGGGTGCGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1167
Db	436	AlaAlaHisTrpLeuAlaCysIleTrpTyrValIleAlaValLysGluTyrGlu-----	453
QY	1168	GAATCCGAGTGCCTGAG-----ATTGGCTGGCTGACGAGCTGGCCCGCGACTGGAG	1221
Db	454	-----TrpPheProGluSerAsnIleGlyTrpLeuGlnLeuLeuAlaGluArg-----	469
QY	1222	ACTCCCTACTACCTGGTGGCGGAGGCCACTGGAGGGAACAGCTCGGCGCAGAGTGAC	1281

Db	469	-----	469
QY	1282	AACTGCAGCAGCAGCAGCGAGCGCCAAACGAGGCGGTGGAGCTGCTGGCGGCCGCTCG	134
Db	470	-----IysAsnAlaSerValAlaIleLeuThrAlaGlu-----	481
QY	1342	CTGGCGCAGCGCTACATCACCTCCCTCTACTTCGCACCTCAGCAGCCTCACCAGCGTGGCG	1401
Db	482	-----ThrTyrSerThrAlaLeuTyrPheThrPheThrSerLeuThrSerValGly	498
QY	1402	TTCGGCAACGTGTCCGCAACACACGAGACACCCAGAGATCTTCTCCATCTGCACCATGCTC	1461
Db	499	PheGlyAsnValSerAlaAsnThrAlaGluLysValPheThrIleIleMetMetLeu	518
QY	1462	ATCGGCGCCTGATGCACGCGGTGGTGTGGGAACGTGACGGCGCATCATCCACCGCATG	1521
Db	519	IleGlyAlaLeuMetHisAlaValPheGlyAsnValThrAlaIleIleGlnArgMet	538
QY	1522	TACGCCCGCGCTTCGTACCAACGCGCAGCGCGCACCTGCAGCTGCAGCTATCATCCGCATC	1581
Db	539	TyrSerArgSerLeuTyrGluSerLysTrpArgAspLeuLysAspPheValAlaLeu	558
QY	1582	CACGATATCCCAAGCCCTCAACGACCGCATGCTGGAGTACTTCCAGGCCACCTGGCGC	1641
Db	559	HisAsnMetProLysGluLeuLysGlnArgIleGluAspTyrPheGlnThrSerTrpSer	578
QY	1642	GTGAACAATGGCATCGACACACCGAGCTGCTGCAGAGCCTCCTGCAGAGCTGCGCGCA	1701
Db	579	LeuSerHisGlyIleAspIleTyrGluThrLeuArgGluPheProGluLeuLeuArgGly	598
QY	1702	GACATGCCATGCACCTGCACAAGGAGTCTCTGCAGCTGCCACTGTTGAGGCGGCCAGC	1761
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QY	1762	CGCGCTGCTCGCGGCACTGTCTCTGGCCCTCGCGCCGCTTCGCAGCGCGGCGGAG	1821
Db	619	GlnGlyCysLeuLysLeuLeuSerLeuHisIleLysThrAsnPheCysAlaProGlyGlu	638
QY	1822	TACCTCATCCACGAGCGATGCCCTGCAGGCCCTACTTGTCTGCTCTGCTCCATG	1881
Db	639	TyrLeuIleHisLysGlyAspAlaLeuAsnTyrIleTyrTyrLeuLysAsnGlySerMet	658
QY	1882	GAGGTGCTCAAGGTGGCAGCGTCCGCGCATCTCTAGGAAGGCGACCTGTATCGCGCTG	1941
Db	659	GluValIleLysAspMetValAlaIleLeuGlyLysLeuValGlySer	678
QY	1942	GAGCTG-----	1947
Db	679	AspIleAsnValHisLeuValAlaThrSerAsnGlyGlnMetThrAlaThrThrAsnSer	698
QY	1948	CCCCGGGGGACAGTGGTGAAGCCCAATGCCGACGTGAAGGGCTGACGTACTGCTGC	2007
Db	699	AlaGlyGlnAspValValArgSerSerAspIleLysAlaLeuThrTyrCysAsp	718
QY	2008	CTGCAGTCTCTCAGCTGGCTGGCTGCAGCAGCCTTGCCTCTGCTACCCCGAGTTGCC	2067
Db	719	LeuLysCysIleHisMetGlyGlyLeuValGluValLeuArgLeuTyrProGluTyrGln	738
QY	2068	CGCGCTTCACTGCTGGCGCTCCGAGGGAGCTCAGCTACAACCTGGTCTGGGGGAGGC	2127
Db	739	GlnGlnPheAlaAsnAspIleGlnHisAspLeuThrCysAsnLeuArgGluGlyTyrGlu	758
QY	2128	TCTGCAGAGGTGGACACCAAGC-----TCCCTCAGCGCGCACAATACC	2169
Db	759	AsnGlnAspSerAspIleGlyProSerPheProLeuProSerIleSerGluAspAspGlu	778
QY	2170	CTTATGTCACCGCTGGAG-----GAGAAGGACAGATGGGAGCAGCGGC	2214
Db	779	AsnArgGluGluAlaGluGluGlyGlyLysGlyGluLysGluAsnGlyGly-----Gly	796
QY	2215	CCC-----ACGTCCTCCGACGCCCGCAGCTGATGACCCCTCC	2250

KW	chromosome 3p21.3-24.3.
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OS	Homo sapiens.
XX	
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FT	Domain
FT	423..442
FT	/label= P_loop
XX	
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XX	
XX	03-FEB-2000.
XX	
XX	21-JUL-1999; 99WO-US16752.
XX	
XX	21-JUL-1998; 98US-0119855.
PR	(MILL-) MILLENNIUM PHARM INC.
XX	
PA	Curtis RAJ;
PI	
XX	
DR	WPI; 2000-182682/16.
DR	N-PSDB; AAZ50453.
XX	
XX	Novel gene encoding potassium channel molecule useful in treating
PT	central nervous system disorders such as Alzheimer's disease, multiple
PT	sclerosis, and schizophrenia
PT	
XX	Claim 9; Fig 2; 144pp; English.
XX	
XX	The present sequence is a partial ERG-like protein 2
CC	(ERG-LP2) which is a member of ERG potassium channel family. This
CC	sequence is a result of initial sequencing of clone j1hbaa042h05 which
CC	was obtained from human brain library. ERG-LP2 gene is mapped to
CC	human chromosome 3p21.3-24.3, between markers WI-4218 and RP-L15_1. It
CC	is predominantly expressed in the brain.
CC	The protein functions as a potassium channel modulator and
CC	has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant,
CC	neuroleptic and nootropic activities. The present sequence is
CC	useful for treating several potassium channel mediated disorders (CNS
CC	disorders) such as Alzheimer's disease, Parkinson's disease, multiple
CC	sclerosis, epilepsy, depression, schizophrenic disorders and amnesia.
XX	
SQ	Sequence 542 AA;
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	Pred. No.: 3,67e-111 Length: 542
	Score: 1832.50 Matches: 351
	Percent Similarity: 77.64% Conservative: 83
	Best Local Similarity: 62.79% Mismatches: 92
	Query Match: 30.10% Indels: 33
	DB: 21 Gaps: 5
	US-09-965-830-1_COPY_6_3257 (1-3252) x AAY44905 (1-542)
QY	1 ATGCCGCCATGGGGGCTCTCTGGCGCTCAGACACCTTCTCTGGACACCATCGCTACG 60
Db	1 MetProValMetIysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY	61 CGGTTCCAGCGGACGACAGCTACTTCGTCTGGGCACGCCCGGAGTGGGGGCTCTTC 120
Db	21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40

1198	QY	CAGGAGCTGGCCGCCCGCAGACTCCCTACCTACCTGTGGGCGGAGGCCAGCTGGA	1257
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396	Db	HISGLUeUGLyLysArgLeuGLuSerProTyr	407
1258	QY	GGAAACAGCTCCGGCCAGAGTGCACAGCAGCAGCGAGGCCAACGGGACGGGG	1317
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408	Db	GlyAsnAsnThr-----	411
1318	QY	CTGGAGCTGTGGGCGGCCGTGCTGGCAGCGCCTACATCACCTCCCTACTACTCGCA	1377
		: : : :	
412	Db	-----LeuGLyGLyProSerIleArgSerAlaTyrIleAlaLeuTyrPheThr	428
1378	QY	CTCAGCAGCCTCACACGCTGGGCTCCGGCAACGTGCGCCACACGGCAGCAGCAGAG	1437
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1438	QY	ATCTTCTCCATCTGCACCATGTCTATCGGCGCCTGTATGCACGCGGTGGTGTGGGAAC	1497
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449	Db	IlePheSerIleCysThrMetLeuIleGLyAlaLeuMethisAlaLeuValPheGLyAsn	468
1498	QY	GTACAGGCCATCATCAGCGCATGTAGCGCCGCGCTTTCTGTACCACAGCCGCGCACGGC	1557
		: : : :	
469	Db	ValThrAlaIleIleGLnArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLys	488
1558	QY	GACCTGGGAGATACATCCGCATCCACCGTATCCCAAGGCCCTCAAGCAGCGCATGCTG	1617
		: : : :	
489	Db	AspLeuLysAspPheIleArgValHisLeuProGLnLeuLysGLnArgMetLeu	508
1618	QY	GAGTACTCTCAGSCCACTGGGCGGTGAACAATGGCATCAGACACCACCGAGCTGCTG	1674
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509	Db	GlutYrPheGLnThrTrpSerValAsnAsnGLyIleAspSerAsnGLuValMet	527

Search completed: May 7, 2003, 15:21:08
Job time : 230.5 secs

